

Copyright (c) 1993 - 2004 Compugen Ltd.	GenCore version 5.1.6	30	38	48.1	270	2	AB1308
OM protein - protein search, using sw model		31	38	48.1	270	2	AB1680
Run on:	June 3, 2004, 15:09:24 ; Search time 13.5 Seconds (without alignments)	32	38	48.1	378	1	ATSY1
Title:	US-08-533-895A-39_COPY_56_70	33	38	48.1	466	2	C89820
Perfect score:	79	34	38	48.1	486	2	T20482
Sequence:	1 QNLISNAPLGQFP 15	35	38	48.1	508	2	A71453
Scoring table:	BLOSUM62	36	38	48.1	1113	2	T14260
Gapopen:	10.0 , Gapext 0.5	37	38	48.1	1115	2	T13955
Searched:	283366 seqs, 96191526 residues	38	38	48.1	1906	1	AB2835
Total number of hits satisfying chosen parameters:	283366	39	38	48.1	2201	2	AH0045
Minimum DB seq length: 0		40	37.5	47.5	136	2	G69440
Maximum DB seq length: 2000000000		41	37.5	47.5	325	2	C83545
Post-processing: Minimum Match 0% Maximum Match 100%		42	37	46.8	154	2	AE0445
		43	37	46.8	195	2	D9757
		44	37	46.8	204	2	AB2283
		45	37	46.8	222	2	D69026
ALIGNMENTS							
RESULT 1							
YRHU1							
N;Alternate name: cresolase; monophenol oxidase; phenolase; tyrosinase							
C;Species: Homo sapiens (man)							
C;Date: 30-Jun-1990 #sequence: GB:M62239; PID:9340033; PMID:602961 NID:9340033; PID:9340035							
C;Accession: A38444; S07760; A33393; A38718; JL0098; A40957; S04760; A60149; B60149; S53							
R;Giebel, L.B.; Strunk, K.M.; Spritz, R.A.							
G;omics 9, 435-445, 1991							
A;Title: Organization and nucleotide sequences of the human tyrosinase gene and a truncated							
A;Reference number: A38444; MUID:91236163; PMID:1903356							
A;Accession: A38444							
A;Molecule type: DNA							
A;Residues: 1-529 <GK>							
A;Cross-references: EMBL:X16073; PIDN:CAA34205..1; PMID:g37507							
R;Tateda, A.; Tomita, Y.; Okinaga, S.; Shibahara, S.							
P;Biochem. Biophys. Res. Commun. 162, 984-990, 1989							
P;Title: Functional analysis of the cDNA encoding human tyrosinase precursor.							
A;Reference number: A33393; MUID:89351001; PMID:2504160							
A;Accession: S07760; PMID:90089403; PMID:2480811							
A;Molecule type: DNA							
A;Residues: 1-273 <KIK>							
A;Cross-references: GB:MP27160							
R;Giebel, L.B.; Tripathi, R.K.; Strunk, K.M.; Hanifin, J.M.; Jackson, C.E.; King, R.A.							
A;Am. J. Hum. Genet. 48, 1159-1167, 1991							
A;Title: Tyrosinase gene mutations associated with type IB ("yellow") oculocutaneous al-							
A;Reference number: A38718; MUID:1241133; PMID:1903391							
A;Accession: A38718							
A;Molecule type: DNA							
A;Residues: 1-32 <TAK>							
A;Cross-references: GB:MP27160							
R;Bouchard, B.; Fuller, B.B.; Vilayabradhi, S.; Houghton, A.N.							
J;Exp. Med. 169, 2029-2042, 1989							
A;Title: Induction of pigmentation in mouse fibroblasts by expression of human tyrosinase							
A;Reference number: JL0098; PMID:89298; PMID:249655							
A;Accession: JL0098							
A;Molecule type: mRNA							
A;Residues: 'GR', 1-178'; 'I', 180-191, 'Y', 193-529 <BOU>							
A;Cross-references: EMBL:Y00819; NID:937538; PIDN:CAA68756..1; PMID:g37509							
R;Chintamani, C.D.; Halabian, R.; Kobayashi, Y.; Witkop Jr., C.J.; Kwon, B.S.							
Proc. Natl. Acad. Sci. U.S.A. 88, 5272-5276, 1991							
A;Title: A single base insertion in the putative transmembrane domain of the tyrosinase							
A;Reference number: A40957; MUID:91271371; PMID:1711223							
A;Accession: A40957							
A;Molecule type: mrna							

A;Residues: 1-165,'I',167-489,'CPAGRACELAVSSQEKAA,' <CHI>  
 A;Cross-references: GB: M74314  
 A;Experimental source: albinos melanocytes  
 A;Note: mutant protein isolated from patient with tyrosinase-negative oculocutaneous albinism; R;Kwon, B.-S.; Haq, A.K.; Pomerantz, S.H.; Halaban, R.  
 Proc. Natl. Acad. Sci. U.S.A. 84: 7473-7477, 1987.  
 A;Title: Isolation and sequence of a cDNA clone for human tyrosinase that maps at the mdA;Reference number: A94185; MUID:88041128; PMID:2823263  
 A;Accession: S04760  
 A;Molecule type: mRNA  
 A;Residues: 'L',2-41,'TGV','46-191,'Y','93-307,'T','309-372,'HVPGT', 379-401,'Q', 403-494,'F  
 A;Cross-references: GB: J03581; NID:930027; PID:AAA61241.1; PID:g3440028  
 A;Experimental source: normal melanocytes  
 A;Note: the sequence differs from that shown in several regions due to reading frame shift  
 R;Wittbjer, A.; Odh, G.; Rosengren, A.M.; Roszman, E.; Roszman, H.  
 Acta Derm. Venereol. 70, 291-294, 1990  
 A;Title: Isolation of soluble tyrosinase from human melanoma cells.  
 A;Reference number: A60149; MUID:9101167; PMID:1977251  
 A;Accession: A60149  
 A;Molecule type: protein  
 A;Residues: 'X',25-28 <WIT>  
 A;Note: the sequence was determined from a soluble form of the enzyme from melanoma cell  
 A;Accession: B60149  
 A;Molecule type: protein  
 A;Residues: 19-23,'X',25-34 <WIT2>  
 A;Cross-references: EMBL: M63238  
 A;Note: the sequence was determined from a membrane-bound form of the enzyme from melanoma cells submitted to the EMBL Data Library, July 1991  
 R;Wittbjer, A.; Dahibaech, B.; Odh, G.; Rosengren, A.M.; Roszman, E.; Roszman, H.  
 Acta Derm. Venereol. 69, 125-131, 1989  
 A;Title: Isolation of human tyrosinase from cultured melanoma cells.  
 A;Description: Organization and nucleotide sequences of the human tyrosinase gene and a  
 A;Reference number: S53560  
 A;Accession: S53560  
 A;Molecule type: protein  
 A;Residues: 396-455 <GI3>  
 A;Cross-references: EMBL: M63238  
 A;Map position: 11q11-11q21  
 A;Introns: 273/3; 346/1; 395/2; 456/1  
 C;Superfamily: monophenol monooxygenase  
 C;Keywords: albinism; copper; glycoprotein; melanin biosynthesis; monooxygenase; oxidoreductase; Nucleic Acids Res. 22, 5446-5455, 1994  
 A;Title: Direct fluorescence analysis of genetic polymorphisms by hybridization with oligonucleotides  
 A;Reference number: S53559; MUID:95116340; PMID:78166339  
 A;Contents: annotation  
 C;Comment: This cell-specific oxidase is a glycoprotein containing two Cu per enzyme; it  
 reactions in the formation of pigments such as melanins and other polyphenolic compound  
 C;Genetics:  
 A;Gene: GBR:TYR  
 A;Cross-references: GDB:120476 ; OMIM:203100  
 A;Map position: 11q11-11q21  
 A;Introns: 273/3; 346/1; 395/2; 456/1  
 C;Keywords: albinism; copper; glycoprotein; melanin biosynthesis; monooxygenase; oxidoreductase; Nucleic Acids Res. 22, 5446-5455, 1994  
 F;19-529;Product: monophenol monooxygenase #status predicted <STG>  
 F;47-500;Domain: transmembrane #status predicted <TM>  
 F;86-111-161-230,331,371;Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;180-202,211;Binding site: copper (His) #status predicted  
 F;363,367,390,420;Binding site: copper (His) #status predicted  
 Query Match 100 0% Score 79; DB 1; Length 529;  
 Best Local Similarity 100 0% Pred. No. 7.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QNILLSNAPLGQQFP 15  
 Db 56 QNILLSNAPLGQQFP 70

**RESULT 3**

YRNCS

monophenol monooxygenase (EC 1.14.18.1) precursor [validated] - mouse

C; Species: *Mus musculus* (house mouse)

C; Accession: A27711; #sequence: 31-Mar-1989 #text change 20-Apr-2000

R; /Kwon, B.S.; Wakulchik, M.; Haq, A.K.; Halaban, R.; Kestler, D.

Biochim. Biophys. Res. Commun. 153, 1301-1309, 1988

A; Title: Sequence analysis of mouse tyrosinase cDNA and the effect of melanotropin on its expression. Reference number: A27711; PMID:3134020

A; Accession: A27711; MUID:88268910;

A; Molecule type: mRNA

A; Residues: 1-1533 <KNO>

A; Cross-references: GB:MA2034; NID:G202247; PID:AAA40516.1; PID:g202248

A; Experimental source: Cloudman S-91 melanoma cells

A; Author: Wakulchik, M.; Kestler, D.; Barton, D.E.; Francke, U.; Lamoreux

J. Invest. Dermatol. 81, 589-594, 1989

A; Title: Isolation, chromosomal mapping, and expression of the mouse tyrosinase gene.

A; Reference number: A60778; PMID:90010220; PMID:2507645

A; Accession: A60778

A; Status: translation not shown

A; Molecule type: DNA

A; Residues: 1-273 <KNO>

A; Experimental source: BALB/c

A; Author: Tabe, L.; Garattini, E.; Sartori, D.; Studer, M.; Mintz, B.

Biochem. Res. Commun. 159, 848-853, 1989

A; Title: Isolation and characterization of variant cDNAs encoding mouse tyrosinase.

A; Reference number: A32429; MUID:89193679; PMID:244997

A; Accession: A32429

A; Molecule type: mRNA

A; Residues: 1-102, 'C', 104-345, 'G', 347-533 <TER>

A; Cross-references: GB:MA24560; NID:9202249; PID:AAA40517.1; PID:g202250

A; Accession: B32429

A; Molecule type: mRNA

A; Residues: 1-77,155-345, 'G', 347-533 <TE2>

A; Cross-references: GB:MA24560

A; Experimental source: B16 melanoma cells

A; Author: Mueller, G.; Ruppert, S.; Schmid, E.; Schuetz, G.

EMBO J. 7, 2723-2730, 1988

A; Title: Functional analysis of alternatively spliced tyrosinase gene transcripts.

A; Reference number: S01170; PMID:82930636; PMID:3141148

A;Cross-references: GB:X12782; NID:955061; PIDN:CAA31273.1; PID:955062  
 R;yamamoto, H.; Takeuchi, S.; Kudo, T.; Nakata, A.; Shinoda, T.; Takeuchi, I.  
 Jpn.; J. Genet. 62, 271-274, 1987  
 A;Title: Cloning and sequencing of mouse tyrosinase cDNA.  
 A;Reference number: S02278  
 A;Accession: S02278  
 A;Molecule type: mRNA  
 A;Residues: 1-105; 'C', '104-263', 'I', '265-345', 'G', '347-448 <YAM>  
 A;Note: part of this sequence was confirmed by protein sequencing  
 R;Shibahara, S.; Okunaga, S.; Tomita, Y.; Takeda, A.; Yamamoto, H.; Sato, M.; Takeuchi, I.  
 Eur. J. Biochem. 189, 455-461, 1990  
 A;Title: A point mutation in the tyrosinase gene of BALB/c albino mouse causing the cysteine residue at position 156 to change to serine.  
 A;Reference number: S15753; MUID:90249393; PMID:2110899  
 A;Accession: S15753  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: DNA  
 A;Residues: 1-13 <SH1>  
 A;Cross-references: EMBL:X51743; NID:955057; PIDN:CAA36033.1; PID:955058  
 A;Experimental source: strain BALB/C  
 R;Kwon, B.S.; Halaban, R.; Chintamani, C.  
 Biochem. Biophys. Res. Commun. 161, 252-260, 1989  
 A;Title: Molecular basis of mouse Himalayan mutation.  
 A;Reference number: I49736; MUID:82273644; PMID:2567165  
 A;Accession: I49736  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: mRNA  
 A;Residues: 1-39; 'I', '41-102', 'C', '104-196', 'Q', '198-245', 'G', '347-419', 'R', '421-533 <RES>  
 A;Cross-references: GB:MM2729; NID:919345; PIDN:AAA37006.1; PID:9302296  
 C;Comment: This cell-specific oxidase is a glycoprotein containing two Cu per enzyme; it  
 reactions in the formation of pigments such as melanins and other polyphenolic compound  
 C;Genetics:  
 A;Gene: Tyrl  
 A;Map Position: 7  
 C;Superfamily: monophenol monooxygenase  
 C;Keywords: alternativ splicing; copper; glycoprotein; melanin biosynthesis;  
 F;1-8/Domain: signal sequence #status predicted <SIG>  
 F;19-53/Domain: monophenol monooxygenase #status predicted <MAT>  
 F;86,111-161,230,337,371/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Best Local Similarity 79.7%; Score 63; DB 1; Length 533;  
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 QNLISNAPLGQFP 15  
 Db 56 QDVLSSAPSQGPQFP 70

RESULT 4  
 JC1392  
 monophenol monooxygenase (EC 1.14.18.1) - Japanese pond frog  
 C;Species: Rana nigromaculata (Japanese pond frog)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 20-Jun-2000  
 C;Accession: JC1392; 151169  
 R;Tokase, M.; Miura, I.; Nakata, A.; Takeuchi, T.; Nishikata, M.  
 Gene 121, 359-363, 1992  
 A;Title: Cloning and sequencing of the cDNA encoding tyrosinase of Japanese pond frog.  
 A;Reference number: JC1392; MUID:93077054; PMID:1446833  
 A;Accession: JC1392  
 A;Molecule type: mRNA  
 A;Residues: 1-532 <TAK>  
 R;Miura, I.; Okamoto, H.; Nakata, A.; Nishioka, M.  
 Jpn.; J. Genet. 70, 79-92, 1995  
 A;Title: Analysis of the tyrosinase gene of the Japanese pond frog, *Rana nigromaculata*:  
 A;Accession: 151169; MUID:95290234; PMID:7772385  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: DNA  
 A;Residues: 1-9; 'A', 11-277 <MIU>

A;Cross-references: GB:D37779; NID:9809507; PIDN:BA007034.1; PID:9809558  
 C;Superfamily: monophenol monooxygenase  
 C;Keywords: Glycoprotein; oxidoreductase; transmembrane protein  
 F;47,90,115,165,234,294,341,360,375/Binding site: carbohydrate (Asn) (covalent) #status  
 Query Match 62.0%; Score 49; DB 2; Length 532;  
 Best Local Similarity 53.3%; Pred. No. 1.4;  
 Matches 8; Conservative 5; Mismatches 2;  
 Qy 1 QNLISNAPLGQFP 15  
 Db 60 QDVLSSAPSQGPQFP 74

RESULT 5  
 A05205  
 hypothetical protein 1708 - common tobacco chloroplast  
 C;Species: chloroplast *Nicotiana tabacum* (common tobacco)  
 C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 11-Apr-1995  
 C;Accession: A05205  
 R;Sugura, M.  
 Submitted to the EMBL Data Library, August 1986  
 A;Reference number: A00149  
 A;Accession: A05205  
 A;Molecule type: DNA  
 A;Residues: 1-1708 <SUG>  
 A;Experimental source: cv. Bright Yellow 4  
 R;Shinozaki, K.; Ohme, M.; Tanaka, M.; Wakasugi, T.; Hayashida, N.; Matsubayashi, T.; Za-Deno, H.; Kanogashira, T.; Yamada, K.; Kusuda, J.; Makaiwa, F.; Kato, A.; Tohodoh, N.; Si-  
 EMBO J. 5, 2043-2049, 1986  
 A;Title: The complete nucleotide sequence of the tobacco chloroplast genome: its gene organization, gene annotation, gene organization, sites, features  
 C;Genetics:  
 A;Genome: chloroplast  
 C;Keywords: chloroplast

Query Match 59.5%; Score 47; DB 2; Length 1708;  
 Best Local Similarity 66.7%; Pred. No. 13;  
 Matches 8; Conservative 2; Mismatches 2;  
 Qy 1 QNLISNAPLG 12  
 Db 1334 QNVLLSNCPIDP 1345

RESULT 6  
 S01446  
 hypothetical protein 2131 - spinach chloroplast  
 C;Species: chloroplast *Spinacia oleracea* (spinach)  
 C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 21-Jul-2000  
 C;Accession: S01446  
 R;Zhou, D.X.; Masseonet, O.; Quigley, F.; Marion, M.J.; Moneger, F.; Huber, P.; Mache, R.  
 Curr. Genet. 1, 433-439, 1988  
 A;Title: Characterization of a large inversion in the spinach chloroplast genome relative to the rice chloroplast genome  
 A;Reference number: S01446; MUID:88235221; PMID:2841033  
 A;Accession: S01446  
 A;Status: translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-2131 <ZER>  
 A;Cross-references: EMBL:X07908; NID:g12245; PIDN:CAA30743.1; PID:912246  
 C;Genetics:  
 A;Genome: chloroplast  
 C;Keywords: chloroplast

Query Match 59.5%; Score 47; DB 2; Length 2131;  
 Best Local Similarity 66.7%; Pred. No. 16;  
 Matches 8; Conservative 2; Mismatches 2;  
 Qy 1 QNLISNAPLG 12  
 Db 1742 QNVLLSNCPIDP 1753

**RESULT 7**  
 S78398 hypothetical protein 2216 - beechdrops plastid  
 C;Species: Plastid *Epifagus virginiana* (beechdrops)  
 C;Date: 25-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 05-Jun-1998  
 C;Accession: S78398; S78304  
 R;Wolfe, K.H.; Morden, C.W.; Emb, S.C.; Palmer, J.D.  
 A;Title: Rapid evolution of the plastid translational apparatus in a nonphotosynthetic plant  
 A;Reference number: S78378; MUID:3021155; PMID:1404416  
 A;Accession: S78398  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-2216 <WOL>  
 A;Cross-references: EMBL: M81884; NID: g336917; PID: g336938  
 A;Genetics: G1  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992  
 A;Accession: S78404  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-2216 <WON>  
 A;Cross-references: EMBL: M81884; NID: g336917; PID: g336938  
 A;Genetics: G2  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992  
 C;Genetics: <G1>  
 A;Gene: 2216\_a  
 C;Genome: plastid  
 C;Genetics: <G2>  
 A;Gene: 2216\_b  
 A;Genome: plastid  
 C;Keywords: plastid

Query Match Score 59.5%; DB 2; Length 2216;  
 Best Local Similarity 66.7%; Pred. No. 17;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGP 12  
 Db 1834 QNILLSNAPLGP 1845

**RESULT 8**  
 D70914 hypothetical protein Rv1425 - Mycobacterium tuberculosis (strain H37RV)  
 C;Species: Mycobacterium tuberculosis  
 C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
 C;Accession: D70914  
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998  
 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome  
 A;Reference number: A70500; MUID: 9825987; PMID: 9634230  
 A;Accession: D70914  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-459 <COL>  
 A;Cross-references: GB: Z95844; GB: ALI23456; NID: g3250713; PID: CAB09245.1; PID: e318877;  
 A;Experimental source: strain H37RV  
 C;Genetics:  
 A;Gene: Rv1425

Query Match Score 52.5%; DB 2; Length 459;  
 Best Local Similarity 57.1%; Pred. No. 25;  
 Matches 8; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy 2 NILLSNAPLGP 15  
 Db 380 NLVYVSNTVP-GPPPPP 392

**RESULT 9**  
 AB2156 hypothetical protein al12801 [imported] - *Nostoc* sp. (strain PCC 7120)  
 C;Species: *Nostoc* sp. PCC 7120  
 A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120  
 C;Date: 14-Dec-2001 #text\_change 09-Dec-2002  
 C;Accession: AB2156  
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi, Nakanishi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.; DNA Res. 8, 205-213, 2001  
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. strain PCC 7120  
 A;Reference number: AB1807; MUID: 21595285; PMID: 11759840  
 A;Accession: AB2156  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-295 <KUR>  
 A;Cross-references: GB: BA000019; PIDN: BAB74500.1; PID: g17131894; GSPDB: GN00179  
 A;Experimental source: strain PCC 7120  
 C;Genetics:  
 A;Gene: al12801

Query Match Score 41%; DB 2; Length 295;  
 Best Local Similarity 77.8%; Pred. No. 18;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 NAPLGPPP 15  
 Db 69 NAPLNPNFPP 77

**RESULT 10**  
 AD1166 probable peptidoglycan bound protein (LPXTG motif) lmo0732 [imported] - *Listeria monocytogenes*  
 C;Species: *Listeria monocytogenes*  
 C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001  
 C;Accession: AD1166  
 R;Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Durand, L.; Dubourget, O.; Entian, K.D.; Fischi, H.; Science 294, 849-852, 2001  
 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurakhat, G.; Maitouram, A.; Makok, C.; Schlueter, T.; Simeos, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A;Title: Comparative Genomics of *Listeria* species  
 A;Reference number: AB1077; MUID: 21537219; PMID: 11679669  
 A;Accession: AD1166  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-638 <GA>  
 A;Cross-references: GB: NC 003210; PIDN: CAC98810.1; PID: g16410121; GSPDB: GN00177  
 A;Experimental source: strain EGD-e  
 C;Genetics:  
 A;Gene: lmo0732

Query Match Score 51.9%; DB 2; Length 638;  
 Best Local Similarity 58.3%; Pred. No. 45;  
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NILLSNAPLGPQ 13  
 Db 300 NVMLDNAPNNPQQ 311

**RESULT 11**  
 D40228 reurexin II-beta Precursor - rat  
 C;Species: *Rattus norvegicus* (Norway rat)  
 C;Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Dec-2002  
 C;Accession: D40228; S27888  
 R;Ushkaryov, Y.A.; Petrenko, A.G.; Geppert, M.; Suedhof, T.C.; Science 257, 50-56, 1992  
 A;Title: Neurexins: synaptic cell surface proteins related to the alpha-latrotoxin recep  
 A;Reference number: A40228; MUID: 92320296; PMID: 1621094  
 A;Accession: D40228

A;Status: preliminary; nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-662 <USH>  
 A;Cross-references: GB:M96377; NID:9205717; PID:9105719  
 A;Note: authors translated GAC for residue 411 as Thr and ACC for residue 412 as Asp  
 C;Keywords: neurexin; EGF homology  
 C;Superfamily: neurexin; EGF homology  
 C;Keywords: alternative splicing; transmembrane protein  
 F;1-47/Domain: signal sequence #status predicted <SG>  
 F;48-662/Domain: neurexin II-beta #status predicted <SG>  
 F;48-662/Product: neurexin II-beta #status predicted <SG>

Query Match	51.9%;	Score 41;	DB 2;	Length 662;	Qy	4 LLSNAPLGQQFP 15	Db	524 LLENPPLGGVP 535	
Best Local Similarity	66.7%;	Pred. No.	47;						
Matches	8;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;

Query Match
 51.9%; | Score 41; | DB 2; | Length 1715; | Qy | 4 LLSNAPLGQQFP 15 | Db | 1577 LLENPPLGGVP 1588 |

Best Local Similarity
 66.7%; | Pred. No. | 1.4e+02; |  |  |  |  |  |

Matches
 8; | Conservative | 0; | Mismatches | 4; | Indels | 0; | Gaps | 0; |

RESULT 14  
 CS4258  
 Transcription factor HNF-3 gamma - mouse  
 N;Alternative names: hepatocyte nuclear factor 3 gamma  
 C;Species: Mus musculus (house mouse)  
 C;Date: 18-Aug-1995 #sequence\_revision 19-Oct-1995 #text\_change 18-Jun-1999  
 C;Accession: C54258; S37186  
 R;Kaeberle, K.H.; Hämisch, H.; Luckow, B.; Schutz, G.  
 A;Title: Genetic and molecular identification of a Drosophila histidine decarboxylase gene  
 A;Reference number: S36337; MUID:93209238; PMID:8096176  
 A;Accession: S36337  
 A;Molecule type: mRNA  
 A;Residues: 1-847 <BUR>  
 A;Cross-references: EMBL:X070644; PID:9287837; PIDN:CAA49989.1; PID:g287838  
 C;Genetics:  
 A;Gene: FlyBase:Hdc  
 A;Cross-references: FlyBase:FBgn0005619  
 C;Superfamily: Drosophila histidine decarboxylase; animal histidine decarboxylase homolog  
 C;Keywords: carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate  
 F;1-470/Domain: animal histidine decarboxylase homology <HDC>  
 F;124/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match	51.9%;	Score 41;	DB 1;	Length 847;	Qy	2 MILLSNAPLGQ 13	Db	500 SILLNSPLSOK 511	
Best Local Similarity	58.3%;	Pred. No.	62;						
Matches	7;	Conservative	4;	Mismatches	1;	Indels	0;	Gaps	0;

Query Match
 50.6%; | Score 40; | DB 1; | Length 353; | Qy | 8 APLGQQFP 15 | Db | 72 APLGPTFP 79 |

Best Local Similarity
 87.5%; | Pred. No. | 33; |  |  |  |  |  |

Matches
 7; | Conservative | 0; | Mismatches | 1; | Indels | 0; | Gaps | 0; |

RESULT 15  
 S35090  
 Transcription factor HNF-3 gamma - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C;Accession: S35090; S339533  
 R;Lai, E.; Prezioso, V.R.; Tao, W.; Chen, W.S.; Darnell, J.E.  
 A;Description: submitted to the EMBL Data Library, January 1993  
 A;Reference number: A39533  
 A;Accession: Hepatocyte nuclear factor 3a belongs to a gene family in mammals that is homologous to the HNF-3 genes  
 A;Residues: S35090  
 A;Accession: S35090  
 A;Molecule type: mRNA  
 A;Residues: 1-354 <LA>  
 A;Cross-references: EMBL:109648; NID:9204624; PIDN:AAA41339.1; PID:g204625  
 R;Lai, E.; Prezioso, V.R.; Tao, W.; Chen, W.S.; Darnell Jr., J.E.  
 A;Title: Genes Dev. 5, 416-427, 1991  
 A;Reference number: A39533  
 A;Accession: A39533  
 A;Molecule type: mRNA  
 A;Residues: 1-1715 <USH>  
 A;Cross-references: GB:M96376; NID:9205714; PID:AAA1707.1; PID:g205716  
 A;Note: authors translated the codon GAC for residue 1464 as Thr and ACC for residue 1465  
 R;Uskaryov, Y.A.; Petranko, A.G.; Geppert, M.; Sudhof, T.C.  
 A;Accession: C40228; MUID:92320296; PMID:1621094  
 A;Description: Neurexins: synaptic cell surface proteins related to the alpha-latrotoxin receptor  
 A;Reference number: S27884  
 A;Accession: S27886  
 A;Molecule type: mRNA  
 A;Residues: 1-1666, 'CRK', 1670, 'PREEKLUFG', 1683-1685, 'GL', 1688, 'LDIA', 1694-1695, 'CCVCRRA'

A;Molecule type: mRNA  
A;Residues: 'W', 23, 'QEDDRTT', 31, 'RQEAYAVLF', 43-44, 'T', 57-115, 'A', 117-354 <LA2>  
A;Cross-references: GB:LG9647  
C;Superfamily: transcription factor HNF-3; fork head DNA-binding domain homology  
C;Keywords: DNA binding; nucleus; transcription regulation  
F;119-210/Domain: fork head DNA-binding domain homology <FHBD>

Query Match	Score	DB	Length
Best Local Similarity	87.5%	1	354
Matches	8	Pred. No.	34
Qy	8 APLGQFP 15	Mismatches	0
Db	72 APLGQFP 79	Indels	1
		Gaps	0

Search completed: June 3, 2004, 15:15:25  
Job time : 14.5 secs

Scoring table:	BLOSUM62			
Gapopen:	10.0 , Gapext:	0.5		
Searched:	141681 seqs, 52070155 residues			
Total number of hits satisfying chosen parameters:	141681			
Minimum DB seq length:	0			
Maximum DB seq length:	2000000000			
Post-processing:	Minimum Match 0% Maximum Match 100%			
Database :	SwissProt_42: Listing first 45 summaries			
Result No.	Score	Query Length	DB ID	Description
1	79	100.0	529	1 TYRO_HUMAN
2	67	84.8	273	1 TYRO_CANFA
3	67	84.8	273	1 TYRO_CONJA
4	67	84.8	273	1 TYRO_TRISTI
5	67	84.8	529	1 TYRO_CHICK
6	63	79.7	533	1 TYRO_MOUSE
7	49	62.0	532	1 TYRO_BANNI
8	47	59.5	2131	1 YCF2_SP10L
9	47	59.5	2216	1 YCF2_EPIV1
10	47	59.5	2280	1 YCF2_TOBAC
11	45	57.0	2294	1 YCF2_ARATH
12	44	55.7	426	1 TIG_CHLTE
13	41.5	52.5	459	1 YE43_MYCTU
14	41	51.9	662	1 NK2B_RAT
15	41	51.9	847	1 DCHS_DROME
16	41	51.9	1715	1 NX2A_HUMAN
17	41	51.9	2067	1 NC05_MOUSE
18	40	50.6	350	1 HN3G_HUMAN
19	40	50.6	353	1 HN3G_MOUSE
20	40	50.6	354	1 HN3G_RAT
21	40	50.6	375	1 ACTG_PENCH
22	40	50.6	666	1 NK2B_HUMAN
23	40	50.6	1712	1 NX2A_HUMAN
24	39	49.4	376	1 ACT1_TRYBB
25	39	49.4	376	1 ACT2_TRYBB
26	39	49.4	376	1 ACT_DEIMA
27	39	49.4	540	1 TYRO_ORYIA
28	39	49.4	1014	1 NANH_CLOSE
29	39	49.4	2298	1 YCF2_LOTOA
30	38.5	48.7	322	1 YD67_MYCPN
31	38.5	48.7	502	1 YH60_MYCTU
32	38.5	48.7	669	1 HPO_DROME
33	38.5	48.7	1218	1 MGPC_MYCPN

- RL J. Exp. Med. 178:489-495 (1993).  
 RN [7] SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT TYR-192.  
 RP MEDLINE=21026558; PubMed=1151699;  
 RX MARTINEZ-ARIAS R., Comas D., Andres A., Abello M.T., Domingo-Roura X.,  
 RA Martínez-Ariás R., Comas D., Andres A., Abello M.T., Domingo-Roura X.,  
 RA Bertranpetti J.;  
 RT "The tyrosinase gene in gorillas and the albinism of 'Snowflake'.";  
 RL *Plasmid Cell Res.* 13:467-470 (2000).  
 RN [8]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE=Skin;  
 RX MEDLINE=21388257; PubMed=12477932;  
 RA Strausberg R.L., Fengold E.A., Grouse L.H., Dergee J.G.,  
 RA Shemmen C.M., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,  
 RA Altschul S.F., Zeeberg B., Bustow K.H., Hsieh F.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Boraldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Bosak S.A., Loquellano N.A., Peterman K.J., Mullany L.S., Jackson C.E.,  
 RA McIwan P.J., Abramson R.D., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fainy J., Heilton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,  
 RA Blakesley R.A.C., Grimeswood J.W., Green E.D., Dickenson M.C.,  
 RA Rodriguez A.C., Grimeswood J.W., Green E.D., Dickenson M.C.,  
 RA Butterfield Y.W., Soderberg E.J., Lu X., Gibbs R.A.,  
 RA Schncher A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [9]  
 RP SEQUENCE OF 1-272 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=90089403; PubMed=24809811;  
 RA Takeuchi A., Tomita Y., Okinaga S., Tagami H., Shibahara S.;  
 RT "Characteristic sequences in the upstream region of the human  
 RT tyrosinase gene.";  
 RL Biochim. Biophys. Acta 1009:283-286 (1989).  
 RN [10]  
 RP SEQUENCE OF 1-32 FROM N.A.  
 RX MEDLINE=9935101; PubMed=2504160;  
 RA Takeuchi A., Tomita Y., Yamamoto H., Takeuchi T., Dei T., Dei T., Watanabe M.;  
 RT "Functional analysis of the cDNA encoding human tyrosinase  
 precursor";  
 RL Biochem. Biophys. Res. Commun. 162:984-990 (1989).  
 RN [11]  
 RP SEQUENCE OF 54-195 FROM N.A.;  
 RX MEDLINE=21082082; PubMed=11214319;  
 RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
 RA O'Brien S.J.;  
 RT "Molecular phylogenetics and the origins of placental mammals.";  
 RL *Nature* 409:614-618 (2000).  
 RN [12]  
 RP REVIEW ON OCA-I VARIANTS.  
 RX MEDLINE=99140254; PubMed=10094567;  
 RA Oetting W.S., King R.A.;  
 RA Oetting W.S., King R.A.;  
 RT "Molecular basis of albinism: mutations and polymorphisms of  
 RT pigment genes associated with albinism.";  
 RL *Hum. Mutat.* 13:99-115 (1999).  
 RN [13]  
 RP REVIEW ON OCA-II VARIANTS.  
 RX MEDLINE=99140254; PubMed=10094567;  
 RA Oetting W.S., King R.A.;  
 RA Oetting W.S., King R.A.;  
 RT "Molecular basis of albinism: mutations and polymorphisms of  
 RT pigment genes associated with albinism.";  
 RL *Hum. Mutat.* 2:1-6 (1993).  
 RN [14]  
 RP REVIEW ON OCA-II VARIANTS.  
 RX MEDLINE=99140254; PubMed=10094567;  
 RA Oetting W.S., King R.A.;  
 RA Oetting W.S., King R.A.;  
 RT "Molecular basis of albinism: mutations and polymorphisms of  
 RT pigment genes associated with albinism.";  
 RL *Hum. Mutat.* 13:99-115 (1999).  
 RN [15] IA oculocutaneous albinism.";  
 RP VARIANT OCA-IIA LEU-81.  
 RX MEDLINE=91238392; PubMed=11970634;  
 RA Giebel L.B., Strunk K.M., King R.A., Hanifin J.M., Spritz R.A.;  
 RT "A frequent tyrosinase gene mutation in classic, tyrosinase-negative  
 (type IIA) oculocutaneous albinism.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3255-3258 (1990).  
 RN [16]  
 RP VARIANTS OCA-IB PHE-275 AND LEU-406.  
 RX MEDLINE=91241133; PubMed=103591;  
 RA Giebel L.B., Tripathi R.K., Strunk K.M., Hanifin J.M., Jackson C.E.,  
 RA King R.A., Spritz R.A.;  
 RT "Tyrosinase gene mutations associated with type IIB ('yellow'  
 RT oculocutaneous albinism.");  
 RL *Am. J. Hum. Genet.* 48:1159-1167 (1991).  
 RN [17]  
 RP ERRATUM.  
 RA Giebel L.B., Tripathi R.K., Strunk K.M., Hanifin J.M., Jackson C.E.,  
 RA King R.A., Spritz R.A.;  
 RL *Am. J. Hum. Genet.* 49:696-696 (1991).  
 RN [18]  
 RP VARIANTS OCA-IIA SER-21; TRP-217; HIS-299; SER-446 AND  
 RX MEDLINE=92351982; PubMed=1642278;  
 RA Tripathi R.K., Strunk K.M., Giebel L.B., Weleber R.G., Spritz R.A.;  
 RT "Tyrosinase gene mutations in type I (tyrosinase-deficient)  
 RT oculocutaneous albinism define two clusters of missense  
 RT substitutions.";  
 RL *Am. J. Med. Genet.* 43:865-871 (1992).  
 RN [19]  
 RP VARIANT OCA-IIA ARG-89.  
 RX MEDLINE=91154384; PubMed=1899321;  
 RA Giebel L.B., Strunk K.M., Hsieh C.-L., Sekhon G.S., Francke U.,  
 RT "Homozygous tyrosinase gene mutation in an American black with  
 RT oculocutaneous albinism. A human homologue to the Siamese cat and the  
 RT Himalayan mouse.";  
 RL *J. Clin. Invest.* 87:1119-1122 (1991).  
 RN [20]  
 RP VARIANT OCA-ITS GLN-422.  
 RX MEDLINE=91154384; PubMed=1900309;  
 RA Giebel L.B., Tripathi R.K., King R.A., Spritz R.A.;  
 RT "A tyrosinase gene missense mutation in temperature-sensitive type I  
 RT oculocutaneous albinism. A human homologue to the Siamese cat and the  
 RT Himalayan mouse.";  
 RL *J. Clin. Invest.* 87:1119-1122 (1991).  
 RN [21]  
 RP VARIANT OCA-IIA GLY-412; TYR-55; THR-206 AND ARG-419.  
 RX MEDLINE=92048465; PubMed=943586;  
 RA King R.A., Mentink M.M., Oetting W.S.;  
 RT "Non-random distribution of missense mutations within the human  
 RT tyrosinase gene in type I (tyrosinase-related) oculocutaneous  
 RT albinism.";  
 RL *Mol. Biol. Med.* 8:19-29 (1991).  
 RN [22]  
 RP VARIANT OCA-IIA TLE-176 AND GLN-217.  
 RX MEDLINE=93138611; PubMed=1487241;  
 RA Oetting W.S., King R.A.;  
 RT "Molecular analysis of type I-A (tyrosinase negative) oculocutaneous  
 RT albinism.";  
 RL *Hum. Genet.* 90:258-262 (1992).  
 RN [23]  
 RP VARIANT OCA-IIA GLN-328; ARG-419 AND LEU-431.  
 RX MEDLINE=94070862; PubMed=1902671;  
 RA Tripathi R.K., Bundey S., Musarella M.A., Droetto S., Strunk K.M.,  
 RA Holmes S.A., Spritz R.A.;  
 RT "Mutations of the tyrosinase gene in Indo-Pakistani patients with type  
 RT I (tyrosinase-deficient) oculocutaneous albinism (OCA).";  
 RL *Am. J. Hum. Genet.* 53:1173-1179 (1993).  
 RN [24]  
 RP VARIANT OCA-IIA ASP-47; CYS-217 DEL; HIS-299 AND LYS-373, AND VARIANTS  
 RP OCA-IB SER-152 AND LYS-294.  
 RX MEDLINE=94175072; PubMed=8128955;

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Query Match      100.0%; Score 79; DB 1; Length 529;
Best Local Similarity 100.0%; Pred. No. 4.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0

```

56 QDIVLSNAPFGPQQFP 70

תְּנַשֵּׁא בְּנֵי כָּל־עֲמָדָה וְבְנֵי כָּל־עֲמָדָה

RESULT 3  
TYRO\_COTJA  
ID TYRO\_COTJA  
AC COTJA

RESULT 2  
 PRO\_CANFA STANDARD; PRT; 273 AA.  
 PRO\_TRO\_CANFA PRT;  
 P54834;  
 01-OCT-1996 (Rel. 34, Created)  
 01-OCT-1996 (Rel. 34, Last sequence update)  
 28-FEB-2003 (Rel. 41, Last annotation update)  
 Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase fragment).

Chordata; Craniata; Vertebrata; Euteleostomi;  
Carnivora; Fissipedia; Canidae; Canis

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<i>Tyrosinase</i>	POTENTIAL.
18	<i>Tyrosinase</i> .
17273	COPPER A (BY SIMILARITY).
180	COPPER A (BY SIMILARITY).
202	(POTENTIAL).
211	(POTENTIAL).
86	(POTENTIAL).
111	(POTENTIAL).
1111	(POTENTIAL).
161	(POTENTIAL).
161	(POTENTIAL).
230	(POTENTIAL).
230	(POTENTIAL).

273

תְּלִימָדָה וְעַמְּדָה בְּבֵית־בְּנֵי־צָדֶקָה

1 ONTISNAPICDODB 15  
Query Match 84.8%;  
Best Local Similarity 80.0%;  
Matches 12; Conservative

Db	RESULT 3	TYRO_COTUA	STANDARD:	PRT:	273 AA.
	ID	Q08470			
	AC	AC_01-0CT-1996 (Rel. 34, Created)			
	DT	01-OCT-1996 (Rel. 34, Last sequence update)			
	DT	01-FEB-2003 (Rel. 41, Last annotation update)			
	DB	Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase) (Fragment).			
	GN	TYR.			
	OS	Coturnix coturnix japonica (Japanese quail).			
	OC	Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi			
	OC	Archosauvia; Aves; Neognathae; Galliformes; Phasianidae; Phasianus.			
	OC	Coturnix.			
	OX	NCBI_TaxID=93934;			
	RN	[1]			
	RP	SEQUENCE FROM N.A.			
	RX	MEDLINE-9318407; PubMed=1292011; Miura H., Sato S., Tanaka M., Yamamoto H., Kudo T., Masuko N., Miura H., Sato S., Takeuchi T.; Tanaka S., Takeuchi S., Shibahara S., Takeuchi T.;			
	RA	Physiology of regulatory regions of vertebrate tyrosinase genes			
	RA	PIGMENT CELL RES 5:284-294 (1992)			
	RT	-1 -FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTION			
	RL	THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLS. CATALYZES THE RATE-LIMITING CONVERSIONS OF TYROSINE DOPA, DOPA TO DOPA-QUINONE AND POSSIBLY 5,6-DIHYDROXYINDOLE			
	CC	INDOLE-5,6 QUINONE.			
	CC	-1 - CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA + DOPAquinone + H(2)O.			
	CC	-1 - COFACTOR: Binds 2 copper ions per subunit.			
	CC	-1 - SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.			
	CC	-1 - SIMILARITY: Belongs to the tyrosinase family.			
	CC	This SWISS-PROT entry is copyright. It is produced through a co-operation between the Swiss Institute of Bioinformatics and the EMBL of the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See <a href="http://www.isb-sib.ch">http://www.isb-sib.ch</a> ) or send an email to license@isb-sib.ch).			
	DR	EMBL: S56788; AAB5510.1-;			
	DR	InterPro: IPR008922; Di-copper_centre.			
	DR	InterPro: IPR02227; Tyrosinase.			
	DR	PFAM: PF00264; tyrosinase_1.			
	DR	PRINTS: PR00092; TYROSINASE.			
	DR	PROSITE: PS00049; TYROSINASE_1; PROSITE: PS00049; TYROSINASE_1; PARTIAL.			
	KW	Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal; Transmembrane; Melanin biosynthesis.			
	KW	POTENTIAL.			
	FT	SIGNAL 1 18			
	FT	CHAIN 1.9 >273			
	FT	METAL 180 180			
	FT	METAL 202 202			
	FT	METAL 211 211			
	FT	CARBONYD 86 86			
	FT	CARBODY 1.1 1.1			
	FT	CARBODY 1.61 161			
	FT	CARBODY 23.0 230			
	FT	NON_TER 27.3 273			
	SQ	SEQUENCE 273 AA; 3149 MW; QEA3DE55BE11EA1 CRC64/			
	Query Match	84.8%	Score: 67;	DB 1;	Length 273;
	Best Local Similarity	86.7%	Pred. No. 0.00027;		
	Matches 13;	Conservative 0;	Mismatches 2;	Indels 0;	
Qy	1	ONITISNAPGPQPP	15		

RESULT 4				
TYRO-TRISI	STANDARD;	PRT;	273 AA.	
ID P55026;				
AC DT 01-OCT-1996	(Rel. 34, Created)			
AC DT 01-OCT-1996	(Rel. 34, Last sequence update)			
AC DT 28-FEB-2003	(Rel. 41, Last annotation update)			
DE Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase)				
DE (Fragment)				
GN TYR.				
OS Trionyx sinensis (Chinese softshell turtle) ( <i>Pelodiscus sinensis</i> ).				
OC Testudine; Cryptodira; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Testudine; Cryptodira; Trionychoidea; Trionychidae; Pelodiscus.				
OX NCBI_TaxID=13735;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=S99; Japonicus; TISSUE=Testis;				
RX RA Yamamoto H., Kudo T., Miura H., Sato S., Tanaka M.,				
RA Tanaka S., Takeuchi S., Shibahara S., Takeuchi T.,				
RT "Phylogeny of regulatory regions of vertebrate tyrosinase genes."				
RL Pigment Cell Res. 5:284-294 (1992).				
CC -!- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC COMPOUNDS.				
CC -!- CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA + DOPA(Dopamine + H(2)O).				
CC -!- COFACTOR: Binds 2 copper ions per subunit.				
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.				
CC -!- SIMILARITY: Belongs to the tyrosinase family.				
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).				
DR EMBL; S56789; AAB25511.1; -.				
DR InterPro; IPR002227; Tyrosinase.				
DR Pfam; PF00264; tyrosinase; 1.				
DR PROSITE; PRO0093; TYROSINASE.				
DR PROSITE; PS00497; TYROSINASE_1; 1.				
DR PROSITE; PS00498; TYROSINASE_2; PARTIAL.				
KW Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal;				
KW Transmembrane; Melanin biosynthesis.				
FT SIGNAL 1 18 POTENTIAL.				
FT CHAIN 19 >73 TYROSINASE.				
FT METAL 180 180 COPPER A (BY SIMILARITY).				
FT METAL 202 202 COPPER A (BY SIMILARITY).				
FT METAL 211 211 COPPER A (BY SIMILARITY).				
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . . ) (POTENTIAL).				
FT CARBOHYD 169 169 N-LINKED (GLCNAC. . . ) (POTENTIAL).				
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . . ) (POTENTIAL).				
FT NON TER 273 273				
SQ SEQUENCE 273 AA; 31136 MW; 9365C76RDB26A625 CRC64;				
Query Match 13, Conservative 84.8%; Score 67; DB 1; Length 273; Matches 13; Conservatve 86.7%; Fred. No. 0.00027; Indels 0; Gaps 0;				
QY 1 QNTLISNAPLGQFP 15				
Db 56 QELLISRAPLGQFP 70				
RESULT 5				
TYRO_CHICK				
ID _TYRO_CHICK STANDARD; PRT; 529 AA.				

FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 529 AA; 60357 MW; 74B46452C3EBF5 CRC64;  
 Query Match Score 67; DB 1; Length 529;  
 Best Local Similarity 86.7%; Pred. No. 0.00057;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QNLLSNAP1GPGQFP 15  
 Db 56 QRIILSQAP1GGPQQFP 70

RESULT 6  
 TYRO\_MOUSE STANDARD; PRT; 533 AA.  
 ID -TYRO\_MOUSE STANDARD;  
 AC P11344;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 28-OCT-2003 (Rel. 41, Last annotation update)  
 DE Tyrosinase precursor (BC 1.14.18.1) (Monophenol monooxygenase)  
 DE (Albino locus protein).  
 GN TYR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 OX Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=IBA/2J;  
 RX MEDLINE=89266910; PubMed=3134020;  
 RA Kwon B. S., Wakulich M., Haq A.K., Halaban R., Kestler D.;  
 RT "Sequence analysis of mouse tyrosinase cDNA and the effect of  
 RT melanotropin on its gene expression.";  
 RT Biochem. Biophys. Res. Commun. 161:252-260(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Imamichi;  
 RX MEDLINE=89273644; PubMed=2567165;  
 RA Kwon B. S., Halaban R., Chintamneni C.;  
 RT "Molecular basis of mouse Bimalayan mutation.";  
 RT Biochem. Biophys. Res. Commun. 161:252-260(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89030636; PubMed=3141148;  
 RA Mueller G., Ruppert S., Schmid E., Schuetz G.;  
 RT "Functional analysis of alternatively spliced tyrosinase gene  
 RT transcripts";  
 RL EMBO J. 7:2723-2730(1988).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89133679; PubMed=2494997;  
 RA Terai M., Takeuchi T., Sartori D., Studer M., Mintz B.;  
 RT "Isolation and characterization of variant cDNAs encoding mouse  
 RT tyrosinase";  
 RT Biochem. Biophys. Res. Commun. 159:848-853(1989).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=STBL/6J;  
 RA Yamamoto H., Takeuchi S., Kudo T., Makino K., Nakata A., Shinoda T.,  
 RA Takeuchi T.;  
 RT "Cloning and sequencing of mouse tyrosinase cDNA.";  
 RL Jpn. J. Genet. 62:271-274(1987).  
 RN [6]  
 RP SEQUENCE OF 1-273 FROM N.A.  
 RX MEDLINE=90212084; PubMed=2517217;  
 RA Yamamoto H., Takeuchi S., Kudo T., Sato C., Takeuchi T.;  
 RT "Melanin production in cultured albino melanocytes transfected with  
 mouse tyrosinase cDNA";  
 RL Jpn. J. Genet. 64:121-135(1989).  
 RN [7]  
 RP VARIANT ALBINO.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=90249393; PubMed=2110899;

RA Shibahara S., Okinaga S., Tomita Y., Takeda A., Yamamoto H., Sato M.,  
 Takeuchi T.;  
 RT "A point mutation in the tyrosinase gene of BALB/c albino mouse  
 causing the cysteine->serine substitution at position 85.";  
 RL Eur. J. Biochem. 189:455-461(1990).  
 RN [8]  
 RP VARIANT CHINCHILLA MICE.  
 RA Beermann F., Ruppert S., Hummler E., Bosch F.X., Mueller G.,  
 RT "rescue of the albino phenotype by introduction of a functional  
 tyrosinase gene into mice.";  
 RL EMBO J. 9:2819-2826(1990).  
 CC -I- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN  
 THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC  
 COMPOUNDS. CATALYZES THE RATE-LIMITING CONVERSIONS OF TYROSINE TO  
 DOPA, DOPA TO DOPONE, AND POSSIBLY 5,6-DIHYDROXYINDOLE TO  
 INDOLE-5,6 QUINONE.  
 CC -I- CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA +  
 DOBAquione + H(2)O.  
 CC -I- COFACTOR: Birds: 2 copper ions per subunit.  
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.  
 CC -I- DISEASE: DEFECTS IN TYR RESULT IN VARIOUS FORMS OF ALBINISM.  
 CC -I- HIMALAYAN STRAIN TYROSINASE IS TEMPERATURE SENSITIVE.  
 CC -I- SIMILARITY: Belongs to the tyrosinase family.  
 CC -I- CAUTION: REF 4 SEQUENCE WAS INCORRECT DUE TO A DELETION OF EXON 3.  
 CC -I- CAUTION: REF 4 SEQUENCE WAS INCORRECT DUE TO A DELETION OF EXON 3.  
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 or send an email to license@isb-sib.ch).  
 CC DR D00440; BAR0341.1;  
 CC DR EMBL; M20234; AAA40516.1; -;  
 CC DR EMBL; M26729; AAA37806.1; -;  
 CC DR EMBL; X12782; CAR31273.1; -;  
 CC DR EMBL; M24560; AAA40517.1; -;  
 CC DR EMBL; D00131; BAR00079.1; -;  
 CC DR EMBL; X51743; CAR36033.1; -;  
 CC DR EMBL; D00439; BAR00340.1; -;  
 CC DR PIR; A27711; YRNCS.  
 CC DR MGD; MG1:98880; Tyr.  
 CC DR InterPro; IPR008922; Di-copper centre.  
 CC DR InterPro; IPR002227; Tyrosinase.  
 CC DR PF00264; tyrosinase.1.  
 CC DR PRINTS; PR00092; TYROSINASE.  
 CC DR PROSITE; PS00497; TYROSINASE\_1.  
 CC DR PROSITE; PS00498; TYROSINASE\_2.  
 CC KW Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal;  
 CC KW Transmembrane; Melanin biosynthesis; Disease mutation; Albinism.  
 CC FT SIGNAL 1 18  
 CC FT DOMAIN 19 533  
 CC FT TRANSMEM 19 476  
 CC FT TRANSMEM 477 497  
 CC FT DOMAIN 498 533  
 CC FT METAL 180 180  
 CC FT METAL 202 202  
 CC FT METAL 211 211  
 CC FT METAL 363 363  
 CC FT METAL 367 367  
 CC FT METAL 390 390  
 CC FT DOMAIN 503 508  
 CC FT CARBOHYD 86 86  
 CC FT CARBOHYD 111 111  
 CC FT CARBOHYD 161 161  
 CC FT CARBOHYD 230 230  
 CC FT CARBOHYD 337 337  
 CC FT CARBOHYD 371 371  
 CC FT VARIANT 103 103  
 CC FT VARIANT 420 420



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IC X07908; CA330743; 1; -.

IC EMBL; AJ400048; CAB88802; 1; -.

IC PIR; S01446; S01446.

IC InterPro; IPR003553; AAA\_ATPase.

IC InterPro; IPR003959; AAA\_ATPase\_centr.

IC InterPro; IPR008543; DUF825.

DR SMART; SM00382; AAA; 1.

DR Chloroplast; Hypothetical protein.

FT CONFLICT 853 853 I -> T (IN REF. 1) :

FT CONFLICT 937 937 K -> N (IN REF. 1) :

FT CONFLICT 973 973 T -> P (IN REF. 1) :

FT CONFLICT 1946 1946 S -> T (IN REF. 1) :

SEQUENCE 2131 AA; 249980 MW; 915CCP87D1C32E31 CRC64;

Query Match 59.5%; Score 47; DB 1; Length 2131;

Best Local Similarity 66.7%; Pred. No. 8.5;

Matches 8; Conservative 2; Mismatches 0;

Gaps 0;

SY 1 QNLLSNAPLG 12

SY 1742 QNVLLNSCPIDP 1753

---

RESULT 9

CC YCF2\_EPIVI

CC YCF2\_BPIVI

CC STANDARD;

CC PRT; 2216 AA.

DC P30072; 01-APR-1993 (Rel. 25, Created)

DC 01-APR-1993 (Rel. 25, Last sequence update)

DC 28-FEB-2003 (Rel. 41, Last annotation update)

DE Hypothetical 259.5 kDa protein ycf2 (ORF 2216).

DE YCF2- AND YCF2-B.

DS Epifagus virginiana (Beechdrops).

NCI Chloroplast; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Lamiaceae; Orobanchaceae; Epifagaceae.

NCI NCBI\_TaxID=4177;

NN [1] N

NN SEQUENCE FROM N.A.

NN MEDLINE#93065301; PubMedId=1332054;

NN Wolfe K.H., Morden C.W., Palmer J.D.;

NN "Function and evolution of a minimal plastid genome from a nonphotosynthetic parasitic plant,"

NN Proc. Natl. Acad. Sci. U.S.A. 89:10648-10652 (1992).

NN !- SIMILARITY: Belongs to the ycf2 family.

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IC EMBL; M81884; AAA5867; 1; -.

IC EMBL; M81884; AAA5873; 1; -.

IC PIR; S78398; S78398.

IC InterPro; IPR003959; AAA\_ATPase\_centr.

IC InterPro; IPR008543; DUF825.

IC Pram; PF00004; AAA; 1.

IC Pfam; PF05695; DUF825; 1.

IC Chloroplast; Hypothetical protein.

SEQUENCE 2216 AA; 259511 MW; E2D9B5A4E9488DFF CRC64;

SY 59.5%; Score 47; DB 1; Length 2216;

Best Local Similarity 66.7%; Pred. No. 8.9;

	Matches	8;	Conservative	2;	Mismatches	2;	Indels	0;	Gaps	0;
Qy		1	QNTILSNAPLGP	12						
Db	1834	QNVILSNCIDP	1845							
<b>RESULT 10</b>										
YCF2	TOBAC	STANDARD;	PRT;	2280	AA.					
ID	YCF2_TOBAC									
AC	P09976; P09977;									
DT	01-MAR-1989 (Rel. 10, Created)									
DT	15-DEC-1998 (Rel. 37, Last sequence update)									
DT	16-OCT-2001 (Rel. 40, Last annotation update)									
DE	Hypothetical 267 kDa protein YCF2 (ORF 2280).									
GN	YCF2.									
OS	Nicotiana tabacum (Common tobacco).									
OG	Chloroplast.									
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;									
OC	Sporomchnophytina; Magnoliophyta; eudicots; core eudicots; asterids;									
OC	Lamiales; Solanales; Solanaceae; Nicotianae.									
NCBI_TaxID	4097;									
RN	[1]									
RP	SEQUENCE FROM N.A.									
RC	STRAIN/ENV. Bright Yellow 4,									
RA	Shinobayashi K., Ohme Zaita M., Tanaka M., Wakasugi T., Hayashida N.,									
RA	Matsumoto K., Ohno C., Chunwongse J., Obokata J., Sugita M.,									
RA	Yamaguchi Shinozaki K., Ono C., Torazawa K., Meng B.-Y., Sugita M.,									
RA	Deno H., Kamogashira T., Yamada J., Kusuda J., Takaiwa F., Kato A.,									
RA	Tobdon N., Shimada H., Sugiyura M.,									
RA	"The complete nucleotide sequence of the tobacco chloroplast genome: its gene organization and expression."									
RT	EMBO J. 5:2043-2049 (1986).									
RL	[2]									
RN	RN									
RP	REVISONS.									
RA	Sugiyura M.									
RL	Submitted (FEB-1998) to the EMBL/Genbank/DBJU databases.									
CC	-1- FUNCTION: Not yet known.									
CC	-1- SIMILARITY: Belongs to the Ycf2 family.									
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires license agreement. (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).									
CC	DR	Z00044; CAA77427.1; -.								
CC	DR	EMBL; 200044; CAA77438.1; -.								
DR	DR	P05204; A05204.								
DR	DR	InterPro; IPR003593; AAA_APbase.								
DR	DR	InterPro; IPR003593; AAA_APbase_centr.								
DR	DR	InterPro; IPR005453; DUF825.								
PFam	DR	PF00004; AAA; 1.								
PFam	DR	PF05635; DUF825; 1.								
SMART	DR	SM00382; AAA; 1.								
KW	KW	Chloroplast; Hypothetical protein.								
SEQUENCE	SQ	SEQUENCE 2280 AA; 266812 MW; E246D5F3D902C06D CRC64;								
Query Match		59.5%								
Best Local Similarity		66.7%								
Matches	8;	Conservative	2;	Mismatches	2;	Indels	2;	Gaps	0;	



RC STRAIN=CDC 1551 / Oshkosh;  
 RX MEDLINE=2220643; PubMed=12218036;  
 RA Fleischmann R.D., Allard D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Unayam L.A., Ermolaeva M., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Khuori H., Gill J., Mikula A.,  
 RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;  
 RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains";  
 RL J. Bacteriol. 184:5479-5490 (2002).  
 CC -!- SIMILARITY: Belongs to the UPF0089 family.  
 CC -----  
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 CC -----  
 DR EMBL; AE000107; AAK45733.1; ALT\_INIT.  
 DR TIGR; MT14.8; -.  
 DR Tuberculiste; Rv1425; -.  
 DR InterPro; IPR004255; -.  
 DR Pfam; PF003007; UPF0089; 1.  
 KW Hypothetical protein; Complete proteome.  
 SEQUENCE 459 AA; 50062 MW; F436dB588562263 CRC64;  
 Query Match Score 41.5; DB 1; Length 459;  
 Best Local Similarity 57.1%; Pred. No. 14.  
 Matches 8; Conservative 3; Mismatches 2; Indels 1; Gaps 1;  
 Qy 2 NILLISNAPLGQPSP 15  
 Db 380 NLYVYSNVP-GPPPPP 392  
 RESULT 14  
 NX2B RAT STANDARD; PRT; 662 AA.  
 AC QC3376;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 1-OCT-2003 (Rel. 42, Last annotation update)  
 DE Neurexin 2-beta precursor (Neurexin II-beta).  
 GN NRXN2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.  
 OX NCBI\_TAXID=10116;  
 RN [1] SEQUENCE FROM N.A.; AND ALTERNATIVE SPlicing.  
 RC STRAIN=Prague-Dawley; TISSUE=Brain;  
 RX MEDLINE=92320296; PubMed=1621094;  
 RA Ushkaroyev Y.A., Petrenko A.G., Gappert M., Suedhof T.C.;  
 RT "Neurexins: synaptic cell surface proteins related to the alpha-  
 RT latrotoxin receptor and laminin.",  
 RL Science 25:50-56 (1992).  
 RN [2] SEQUENCE OF N-TERMINUS.  
 RC TISSUE=Brain;  
 RX MEDLINE=94216308; PubMed=8163501;  
 RA Ushkaroyev Y.A., Harai Y., Ichchenko K., Moomaw C., Afendis S.,  
 RA Slaughter C.A., Suedhof T.C.;  
 RT "Conserved domain structure of beta-neurexins. Unusual cleaved signal  
 RT sequences in receptor-like neuronal cell-surface proteins.",  
 RL J. Biol. Chem. 269:11987-11992 (1994).  
 RN [3] INTERACTION WITH CASK.  
 RP MEDLINE=96256615; PubMed=8786425;  
 RX Hata Y., Butz S., Suedhof T.C.;  
 RA -----  
 RT "CASK: a novel dlg/PSP95 homolog with an N-terminal calmodulin-dependent protein kinase domain identified by interaction with neurexins.";  
 RT J. Neurosci. 16:2488-2494 (1996).  
 [4] INTERACTION WITH NLGN1; NLGN2 AND NLGN3.  
 RP MEDLINE=96162010; PubMed=8576240;  
 RX RA Ichchenko K., Nguyen T., Suedhof T.C.;  
 RT "Structures, alternative splicing, and neurexin binding of multiple  
 RT neurexins";  
 RT J. Biol. Chem. 271:2676-2682 (1996).  
 RL J. Biol. Chem. 271:2676-2682 (1996).  
 CC -!- FUNCTION: Neuronal cell surface protein that may be involved in  
 CC cell recognition and cell adhesion.  
 CC -!- SUBCELLULAR LOCATION: The cytoplasmic C-terminal region binds to CASK. Isoforms  
 CC Beta 4b bind alpha-dystroglycan and neurologins NLGN1, NLGN2 and  
 NLGN3.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative Promoter;  
 CC Comment=A number of isoforms, alpha-type and beta-type (shown  
 here), are produced by use of alternative promoters. Beta-type  
 isoforms differ from alpha-type isoforms in their N-terminus;  
 CC Event-Alternative splicing; Named isoforms=B;  
 CC Comment=There is a combination of two alternatively spliced  
 extracellular domains at sites 4 and 5 and a cytoplasmic domain  
 at site 6 which are shared with alpha isoforms (AC Q63374) and  
 Beta 4b which are shared independently. Experimental confirmation may be  
 CC needed to be used independently.  
 CC Lacking for some isoforms;  
 CC Name=1; Synonyms=Beta 4A5A;  
 CC IsoId=Q63376-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Beta 4A5B;  
 CC IsoId=Q63376-2; Sequence=VSP\_003519;  
 CC Name=3; Synonyms=Beta 4B5A;  
 CC IsoId=Q63376-3; Sequence=VSP\_003518;  
 CC Name=4; Synonyms=Beta 4B5B;  
 CC IsoId=Q63376-4; Sequence=VSP\_003518, VSP\_003519;  
 CC Name=5; Synonyms=Beta 4A5A6;  
 CC IsoId=Q63376-5; Sequence=VSP\_003520;  
 CC Name=6; Synonyms=Beta 4A5B6;  
 CC IsoId=Q63376-6; Sequence=VSP\_003519, VSP\_003520;  
 CC Name=7; Synonyms=Beta 4B5A6;  
 CC IsoId=Q63376-7; Sequence=VSP\_003518, VSP\_003520;  
 CC Name=8; Synonyms=Beta 4B5B6;  
 CC IsoId=Q63376-8; Sequence=VSP\_003518, VSP\_003519, VSP\_003520;  
 CC -!- TISSUE SPECIFICITY: Brain (neuronal synapse).  
 CC -!- SIMILARITY: Contains 1 laminin G-like domain.  
 CC -!- SIMILARITY: Belongs to the neurexin family.  
 CC -----  
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 CC -----  
 DR EMBL; M96377; AAA41708.1; -.  
 DR HSSP; D4022B; D4022B.  
 DR InterPro; IPR003885; ConA\_like\_lec\_g1.  
 DR InterPro; IPR001791; Laminin\_G.  
 DR SMART; SM00294; 4.1m/1.  
 DR SMART; SM00282; LamG; 1.  
 DR PROSITE; PS00025; LAM G DOMAIN; 1.  
 KW Signal; Transmembrane; Cell adhesion; Glycoprotein;  
 KW Neurexin-like.  
 KW Alternative splicing; Alternative promoter usage.  
 FT SIGNAL 1 46  
 FT CHAIN 47 662 NEUREXIN 2-BETA.  
 FT DOMAIN 47 586 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 587 607 POTENTIAL.  
 FT DOMAIN 608 662 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 87 87 LAMININ G-LIKE.

Query Match 51.9%; Score 41; DB 1; Length 847;  
 Best Local Similarity 58.3%; Pred. No. 34;  
 Matches 7; Conservative 4; Mismatches 1; Indels 0;  
 Gaps 0;

Qy 2 NLLSNAPLGPO 13  
 Db 500 SLLSNPLSPK 511

Search completed: June 3, 2004, 15:14:45  
 Job time : 11 sec(s)

FT DOMAIN 318 321 POLY-THR.  
 FT DOMAIN 324 327 POLY-THR.  
 FT DOMAIN 394 397 POLY-PRO.  
 FT VARSPLIC 594 597 POLY-ALA.  
 FT DOMAIN 203 232 Missing (in isoform 3, isoform 4, isoform 7 and isoform 8).  
 FT VARSPLIC 368 385 Missing (in isoform 2, isoform 4, isoform 6 and isoform 8).  
 FT FTID=VSP 00319. DEGQYQDOSRNTINSNSAQSNGAVKEKAAPAKTPSKAKK  
 FT NDKEKEYVY -> CRKSPPREKLPGSAAGLGLALARCCVC  
 FT RCPATCTACKPLBERGGGRGERGRQMLYTKNK (in  
 FT isoform 5, isoform 6, isoform 7 and  
 FT isoform 8). FTID=VSP 003220.

FT SQ SEQUENCE 662 AA; 70546 MW; A162BFF185FB56B CRC64;

Query Match 51.9%; Score 41; DB 1; Length 662;  
 Best Local Similarity 66.7%; Pred. No. 26;  
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 LLSENAPLGQFP 15  
 Db 524 LLENPPLGPQFP 535

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RESULT 15

DCHS_DROME	STANDARD;	PRT;	847 AA.
ID DCHS_DROME			
AC Q05733;			
DT 01-JUN-1994	(Rel. 29, Created)		
DT 01-JUN-1994	(Rel. 29, Last sequence update)		
DB Histidine decarboxylase (EC 4.1.1.22) (HDC).			
GN HDC.			
OS Drosophila melanogaster (Fruit fly).			
OC Eukaryota; Metazoa; Archipoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oligocephala; Drosophilidae; Drosophila.			
OC NCBITaxon:7227;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=33209238; PubMed=8096176;			
RA Burg M.G., Sarthy P.V., Kollant G.; Pak W.L.;			
RT "Genetic and molecular identification of a Drosophila histidine decarboxylase gene required in photoreceptor transmitter synthesis.";			
RL EMBO J. 12:911-919(1993).			
CC -!- FUNCTION: Required in photoreceptor transmitter synthesis.			
CC -!- CATALYTIC ACTIVITY: L-histidine = histamine + CO(2).			
CC -!- COFACTOR: Pyridoxal phosphate.			
CC -!- SUBUNIT: Homodimer (by similarity).			
CC -!- SIMILARITY: Belongs to the group II decarboxylase family.			

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DR EMBL; X70644; CAA49989.1; -  
 DR S36337; S36337;  
 DR FlyBase; Prgn0005619; Hdc.  
 DR InterPro; IPR002129; Pyridoxal deC.  
 DR PFAM; PF0082; pyridoxal deC; 1.  
 DR PRINTS; PRO0800; YHDERBOXLASE.  
 DR PROSITE; PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 KW Lyase; Decarboxylase; Catecholamine biosynthesis; Pyridoxal phosphate.  
 FT BINDING 304 304 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 SQ SEQUENCE 847 AA; 94106 MW; 6DFDDDE7B3034BC8F CRC64;

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OM protein - protein search, using sw model

Run on: June 3, 2004, 15:09:24 ; Search time 36.5 Seconds

(without alignments)  
129.665 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_56\_70

Perfect score: 79

Sequence: 1 QNILLSNAPLGPQFP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315510202 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRMBL\_25:\*

1: sp\_archea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rabbit:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_virus:\*

16: sp\_bacterioplasm:\*

17: sp\_archaea:\*

#### ALIGNMENTS

RESULT 1  
Q9BEP2

ID Q9BEP2

AC Q9BEP2;

DT 01-JUN-2001 (T-TBMLrel. 17, Created)

DT 01-JUN-2001 (T-TBMLrel. 17, Last sequence update)

DT 01-OCT-2003 (T-TBMLrel. 25, Last annotation update)

DB Tyrosinase (Fragment).

GN TYR.

OS Atelopus fusciceps (Brown-headed spider monkey).

OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrhini; Cebidae; Atelinae; Atelles.

OC NCBI\_TaxID:9508;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21082082; PubMed=11214319;

RA Murphy W.J.; Ezizrik E.; Johnson W.B.; Zhang Y.P.; Ryder O.A., O'Brien S.J.; O'Brien S.J.; RT "Molecular phylogenetics and the origins of placental mammals."

RL Nature 409:614-618 (2001).

DR EMBL:AY012015; AAC:G38758; 1;

DR GO:GO:0016491; P:oxidoreductase activity; IEA.

DR GO:GO:0005198; P:structural molecule activity; IEA.

DR InterPro; IPR008922; Di-copper\_centre.

DR InterPro; IPR006209; EGF\_Like.

DR InterPro; IPR002049; Lanatin\_EGF.

DR InterPro; IPR002227; Tyrosinase.

DR Pfam; PF00264; tyrosinase\_1.

DR PROSITE; PS00022; EGF\_1\_1.

DR PROSITE; PS01249; LAMININ\_TYPE\_EGF; 1.

FT NON\_TER 1

FT NON\_TER 142

SQ SEQUENCE 142 AA;

RN 16198 MW;

NCBI\_TaxID:9508;

Query Match Score 79; DB 6;

Best Local Similarity 100.0%; Pred. No. 3.8e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No. Score Query Match Length DB ID Description

% SUMMARIES					
Result No.	Score	Query	Match	Length	DB ID Description
1	79	100.0	142	6	Q9BEP2 atelopus fusciceps
2	79	100.0	142	6	Q9BEP0 hylobates c
3	79	100.0	142	6	Q9BEP1 macaca mula
4	79	100.0	388	6	Q9GIU6 gorilla gorilla
5	79	100.0	388	6	Q9GIU8 pygathrix nigripes
6	79	100.0	388	6	Q9GIU6 pygathrix nigripes
7	79	100.0	388	6	Q9GIU6 pygathrix nigripes
8	79	100.0	388	6	Q9GIU2 papio hamadryas
9	79	100.0	388	6	Q9GIU4 pygathrix nigripes
10	79	100.0	388	6	Q9GIU6 macaca thibetana
11	79	100.0	388	6	Q9GIU6 trachypithecus obscurus
12	79	100.0	388	6	Q9GIU6 trachypithecus obscurus
13	79	100.0	388	6	Q9GIU2 papio hamadryas
14	79	100.0	388	6	Q9GIU4 macaca nemestrina
15	79	100.0	388	6	Q9GIU4 nasalis larvatus
16	79	100.0	388	6	Q9GIU8 pygathrix nigripes



DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Tyrosinase (EC 1.14.18.1) (Fragment).  
OS Pygathrix nemaeus (Dove langur).  
RT "Molecular evolution (SEP-1999) to the EMBL/GenBank/DBJ databases."  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF133656; AAG7282.1; -;  
DR EMBL; AF133655; AAG7282.1; JOINED.  
DR GO; GO:0004503; F: monophenol monooxygenase activity; IEA.  
DR GO; GO:0016491; F: oxidoreductase activity; IEA.  
DR GO; GO:005198; F: structural molecule activity; IEA.  
DR InterPro; IPR008922; Di-copper\_centre.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR002049; Laminin\_EGF.  
DR InterPro; IPR002227; Tyrosinase.  
DR Pfam; PF0064; Tyrosinase; 1.  
DR PRINTS; PR00022; TYROSINASE.  
DR PROSITE; PS00022; EGF 1..1.  
DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 1..1.  
DR PROSITE; PS00497; TYROSINASE\_1..1.  
DR KW Oxidoreductase.  
FT NON\_TER 388 AA; 43676 MW;  
SQ SEQUENCE 2F1099100E6D9A77 CRC64;

Query Match 100.0%; Score 79; DB 6; Length 388;  
Best Local Similarity 100.0%; Pred. No. 1..1e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQFP 15  
Db 56 QNILLSNAPLGQFP 70

RESULT 7  
Q9GLIV0 PRELIMINARY; PRT; 388 AA.  
ID Q9GLIV0;  
AC Q9GLIV0;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DR Tyrosinase (BC 1.14.18.1) (Fragment).  
OS Pan troglodytes (Chimpanzee).  
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
OC Mammalia; Butheria; Primates; Catarriini; Hominidae; Pan.  
NCBI\_TaxID=9598;  
RN [1] \_TAXID=9598;  
RN SEQUENCE FROM N.A.  
RP SEQUENCE FROM N.A.  
RA Ding B.; Ryder O.A.; Shi P.; Zhang Y.-P.;  
RT "Molecular evolution of tyrosinase gene in primates.";  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF183520; AAG26322.1; -;  
DR EMBL; AF183522; AAG26322.1; JOINED.  
DR GO; GO:0004503; F: monophenol monooxygenase activity; IEA.  
DR GO; GO:0016491; F: oxidoreductase activity; IEA.  
DR GO; GO:005198; F: structural molecule activity; IEA.  
DR InterPro; IPR008922; Di-copper\_centre.  
DR InterPro; IPR002049; EGF\_1..1.  
DR InterPro; IPR002227; Tyrosinase.  
DR Pfam; PF00264; tyrosinase; 1.  
DR PRINTS; PR00022; EGF 1..1.  
DR PROSITE; PS00022; TYROSINASE.  
DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 1..1.  
DR PROSITE; PS00497; TYROSINASE\_1..1.  
DR KW Oxidoreductase.  
FT NON\_TER 388 AA; 43865 MW;  
SQ SEQUENCE 168AEGF17CC5C52B CRC64;

Query Match 100.0%; Score 79; DB 6; Length 388;  
Best Local Similarity 100.0%; Pred. No. 1..1e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQFP 15  
Db 56 QNILLSNAPLGQFP 70

RESULT 8  
Q9GLIV2 PRELIMINARY; PRT; 388 AA.  
ID Q9GLIV2;  
AC Q9GLIV2;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DR Tyrosinase (BC 1.14.18.1) (Fragment).  
OS Pario hamadryas (Hamadryas baboon).  
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
OC Mammalia; Butheria; Primates; Catarriini; Cercopithecidae;  
OC Cercopithecinae; Papio.  
NCBI\_TaxID=9557;  
RN [1]

RESULT 9  
Q9GLIV3 PRELIMINARY; PRT; 388 AA.  
ID Q9GLIV3;  
AC Q9GLIV3;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DR Tyrosinase (BC 1.14.18.1) (Fragment).  
OS Pario hamadryas (Hamadryas baboon).  
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
OC Cercopithecinae; Papio.  
NCBI\_TaxID=9557;

SEQUENCE FROM N.A.  
RA Ding B.; Ryder O.A.; Shi P.; Zhang Y.-P.;  
RT "Molecular evolution of tyrosinase gene in primates.";  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF183636; AAG27274.1; -;  
DR EMBL; AF183634; AAC27274.1; JOINED.  
DR GO; GO:0016491; F: oxidoreductase activity; IEA.  
DR GO; GO:005198; F: structural molecule activity; IEA.  
DR InterPro; IPR008922; Di-copper\_centre.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR002049; Laminin\_EGF.  
DR InterPro; IPR002227; Tyrosinase.  
DR Pfam; PF00264; tyrosinase; 1.  
DR PRINTS; PR00022; EGF 1..1.  
DR PROSITE; PS00022; TYROSINASE.  
DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 1..1.  
DR PROSITE; PS00497; TYROSINASE\_1..1.  
DR KW Oxidoreductase.  
FT NON\_TER 388 AA; 43865 MW;  
SQ SEQUENCE 168AEGF17CC5C52B CRC64;

Query Match 100.0%; Score 79; DB 6; Length 388;  
Best Local Similarity 100.0%; Pred. No. 1..1e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQFP 15  
Db 56 QNILLSNAPLGQFP 70

SEQUENCE FROM N.A.	Matches	15;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Ding B., Ryder O.A., Shi P., Zhang Y.-P.; "Molecular evolution of tyrosinase gene in primates."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.	Qy	1	QNILLSNAPLGQFP	15						
EMBL; AF18385; AAG21892.1; JOINED.	Db	56	QNILLSNAPLGQFP	70						
RESULTS 10										
SEQUENCE FROM N.A.										
Ding B., Ryder O.A., Shi P., Zhang Y.-P.; "Molecular evolution of tyrosinase gene in primates."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.	Q9GM6	PRELIMINARY;	PRT;	388 AA.						
EMBL; AF18385; AAG21892.1; JOINED.	ID	Q9GM6;								
GO; GO:004503; F:monophenol monooxygenase activity; IEA.	AC	Q9GM6;								
GO; GO:0016491; F:oxidoreductase activity; IEA.	DT	01-MAR-2001 (TREMBLrel. 16, Created)								
GO; GO:0005198; F:structural molecule activity; IEA.	DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)								
GO; GO:008152; P:metabolism; IEA.	DR	01-OCT-2003 (TREMBLrel. 25, Last annotation update)								
InterPro; IPR008922; Di-copper_centre.	DR	Tyrosinase (EC 1.14.18.1) (Fragment).								
InterPro; IPR006209; EGFR like.	DR	Macaca thibetana (Pere David's macaque).								
InterPro; IPR002227; Tyrosinase.	DR	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Cercopithecinae; Macaca.								
PFam; PF00264; tyrosinase_1.	OS									
PRINTS; PR00092; TYROSINASE.	OC									
PROSITE; PS00022; EGF_1..1.	OC									
PROSITE; PS01248; LANTIN_TYPE_EGF_1..1.	OC									
PROSITE; PS00497; TYROSINASE_1..1.	OX									
Oxidoreductase.	RN	[1]								
NON_TER 388 SEQUENCE 388 AA; 43728 MW; A6B7D85119D526FA CRC64;	RP	SEQUENCE FROM N.A.								
InterPro; IPR008922; Di-copper_centre.	RA	Ding B., Ryder O.A., Shi P., Zhang Y.-P.; "Molecular evolution of tyrosinase gene in primates."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.								
InterPro; IPR006209; EGFR like.	RL	DR								
InterPro; IPR002227; Tyrosinase.	DR	Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.								
PFam; PF00264; tyrosinase_1.	DR	EMBL; AF183651; AAG21044.1; -.								
PRINTS; PR00092; TYROSINASE.	DR	EMBL; AF183660; AAG21044.1; JOINED.								
PROSITE; PS00022; EGF_1..1.	DR	GO; GO:0004503; F:monophenol monooxygenase activity; IEA.								
PROSITE; PS01248; LANTIN_TYPE_EGF_1..1.	DR	GO; GO:0016491; F:oxidoreductase activity; IEA.								
PROSITE; PS00497; TYROSINASE_1..1.	DR	GO; GO:0008152; P:metabolism; IEA.								
Oxidoreductase.	DR	InterPro; IPR006209; EGFR like.								
NON_TER 388 SEQUENCE 388 AA; 43718 MW; 1196D52193651044 CRC64;	FT	InterPro; IPR002049; Lammin_EGF.								
NON_TER 388 SEQUENCE 388 AA; 43718 MW; 1196D52193651044 CRC64;	SQ	DR								
RESULTS 9										
SEQUENCE FROM N.A.										
Ding B., Ryder O.A., Shi P., Zhang Y.-P.; "Molecular evolution of tyrosinase gene in primates."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.	Q9GLS4	PRELIMINARY;	PRT;	388 AA.						
EMBL; AF183671; AAG29389.1; JOINED.	ID	Q9GLS4;								
GO; GO:004503; F:monophenol monooxygenase activity; IEA.	AC	Q9GLS4;								
GO; GO:0016491; F:oxidoreductase activity; IEA.	DT	01-MAR-2001 (TREMBLrel. 16, Created)								
GO; GO:0005198; F:structural molecule activity; IEA.	DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)								
GO; GO:008152; P:metabolism; IEA.	DR	01-OCT-2003 (TREMBLrel. 25, Last annotation update)								
InterPro; IPR008922; Di-copper_centre.	DR	Tyrosinase (EC 1.14.18.1) (Fragment).								
InterPro; IPR006209; EGFR like.	DR	Pygathrix roxellana (Golden snub-nosed monkey).								
InterPro; IPR002227; Tyrosinase.	DR	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Colobinae; Pygathrix.								
PFam; PF00264; tyrosinase_1.	OS									
PRINTS; PR00092; TYROSINASE.	OC									
PROSITE; PS00022; EGF_1..1.	OC									
PROSITE; PS01248; LANTIN_TYPE_EGF_1..1.	OC									
Oxidoreductase.	RN	[1]								
SEQUENCE FROM N.A.										
Ding B., Ryder O.A., Shi P., Zhang Y.-P.; "Molecular evolution of tyrosinase gene in primates."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.	Q9GLS0	PRELIMINARY;	PRT;	388 AA.						
EMBL; AF183670; AAG29389.1; JOINED.	ID	Q9GLS0;								
GO; GO:004503; F:monophenol monooxygenase activity; IEA.	AC	Q9GLS0;								
GO; GO:0016491; F:oxidoreductase activity; IEA.	DT	01-MAR-2001 (TREMBLrel. 16, Created)								
GO; GO:0005198; F:structural molecule activity; IEA.	DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)								
GO; GO:008152; P:metabolism; IEA.	DR	01-OCT-2003 (TREMBLrel. 25, Last annotation update)								
InterPro; IPR008922; Di-copper_centre.	DR	Tyrosinase (EC 1.14.18.1) (Fragment).								
InterPro; IPR006209; EGFR like.	DR	Trachypithecus leucocebus.								
InterPro; IPR002227; Tyrosinase.	DR	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Colobinae; Trachypithecus.								
PFam; PF00264; tyrosinase_1.	OS									
PRINTS; PR00092; TYROSINASE.	OC									
PROSITE; PS00022; EGF_1..1.	OC									
PROSITE; PS01248; LANTIN_TYPE_EGF_1..1.	OC									
Oxidoreductase.	RN	[1]								
SEQUENCE FROM N.A.										
Ding B., Ryder O.A., Shi P., Zhang Y.-P.; "Molecular evolution of tyrosinase gene in primates."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.	Q9GLS0	PRELIMINARY;	PRT;	388 AA.						
EMBL; AF183681; AAG33680.1; JOINED.	ID	Q9GLS0;								
GO; GO:004503; F:monophenol monooxygenase activity; IEA.	AC	Q9GLS0;								
GO; GO:0016491; F:oxidoreductase activity; IEA.	DT	01-MAR-2001 (TREMBLrel. 16, Created)								
GO; GO:0005198; F:structural molecule activity; IEA.	DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)								
GO; GO:008152; P:metabolism; IEA.	DR	01-OCT-2003 (TREMBLrel. 25, Last annotation update)								
InterPro; IPR008922; Di-copper_centre.	DR	Tyrosinase (EC 1.14.18.1) (Fragment).								
InterPro; IPR006209; EGFR like.	DR	Trachypithecus leucocebus.								
InterPro; IPR002227; Tyrosinase.	DR	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Colobinae; Trachypithecus.								
PFam; PF00264; tyrosinase_1.	OS									
PRINTS; PR00092; TYROSINASE.	OC									
PROSITE; PS00022; EGF_1..1.	OC									
PROSITE; PS01248; LANTIN_TYPE_EGF_1..1.	OC									
Oxidoreductase.	RN	[1]								
SEQUENCE FROM N.A.										
Ding B., Ryder O.A., Shi P., Zhang Y.-P.; "Molecular evolution of tyrosinase gene in primates."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.	Q9GLS0	PRELIMINARY;	PRT;	388 AA.						
EMBL; AF183681; AAG33680.1; JOINED.	ID	Q9GLS0;								
GO; GO:004503; F:monophenol monooxygenase activity; IEA.	AC	Q9GLS0;								
GO; GO:0016491; F:oxidoreductase activity; IEA.	DT	01-MAR-2001 (TREMBLrel. 16, Created)								
GO; GO:0005198; F:structural molecule activity; IEA.	DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)								
GO; GO:008152; P:metabolism; IEA.	DR	01-OCT-2003 (TREMBLrel. 25, Last annotation update)								
InterPro; IPR008922; Di-copper_centre.	DR	Tyrosinase (EC 1.14.18.1) (Fragment).								
InterPro; IPR006209; EGFR like.	DR	Trachypithecus leucocebus.								
InterPro; IPR002227; Tyrosinase.	DR	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Colobinae; Trachypithecus.								
PFam; PF00264; tyrosinase_1.	OS									
PRINTS; PR00092; TYROSINASE.	OC									
PROSITE; PS00022; EGF_1..1.	OC									
PROSITE; PS01248; LANTIN_TYPE_EGF_1..1.	OC									
Oxidoreductase.	RN	[1]								
SEQUENCE FROM N.A.										
Ding B., Ryder O.A., Shi P., Zhang Y.-P.; "Molecular evolution of tyrosinase gene in primates."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.	Q9GLS0	PRELIMINARY;	PRT;	388 AA.						
EMBL; AF183681; AAG33680.1; JOINED.	ID	Q9GLS0;								
GO; GO:004503; F:monophenol monooxygenase activity; IEA.	AC	Q9GLS0;								
GO; GO:0016491; F:oxidoreductase activity; IEA.	DT	01-MAR-2001 (TREMBLrel. 16, Created)								
GO; GO:0005198; F:structural molecule activity; IEA.	DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)								
GO; GO:008152; P:metabolism; IEA.	DR	01-OCT-2003 (TREMBLrel. 25, Last annotation update)								
InterPro; IPR008922; Di-copper_centre.	DR	Tyrosinase (EC 1.14.18.1) (Fragment).								
InterPro; IPR006209; EGFR like.	DR	Trachypithecus leucocebus.								
InterPro; IPR002227; Tyrosinase.	DR	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Colobinae; Trachypithecus.								
PFam; PF00264; tyrosinase_1.	OS									
PRINTS; PR00092; TYROSINASE.	OC									
PROSITE; PS00022; EGF_1..1.	OC									
PROSITE; PS01248; LANTIN_TYPE_EGF_1..1.	OC									
Oxidoreductase.	RN	[1]								
SEQUENCE FROM N.A.										
Ding B., Ryder O.A., Shi P., Zhang Y.-P.; "Molecular evolution of tyrosinase gene in primates."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.	Q9GLS0	PRELIMINARY;	PRT;	388 AA.						
EMBL; AF183681; AAG33680.1; JOINED.	ID	Q9GLS0;								
GO; GO:004503; F:monophenol monooxygenase activity; IEA.	AC	Q9GLS0;								
GO; GO:0016491; F:oxidoreductase activity; IEA.	DT	01-MAR-2001 (TREMBLrel. 16, Created)								
GO; GO:0005198; F:structural molecule activity; IEA.	DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)								
GO; GO:008152; P:metabolism; IEA.	DR	01-OCT-2003 (TREMBLrel. 25, Last annotation update)								
InterPro; IPR008922; Di-copper_centre.	DR	Tyrosinase (EC 1.14.18.1) (Fragment).								
InterPro; IPR006209; EGFR like.	DR	Trachypithecus leucocebus.								
InterPro; IPR002227; Tyrosinase.	DR	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Colobinae; Trachypithecus.								
PFam; PF00264; tyrosinase_1.	OS									
PRINTS; PR00092; TYROSINASE.	OC									
PROSITE; PS00022; EGF_1..1.	OC									
PROSITE; PS01248; LANTIN_TYPE_EGF_1..1.	OC									
Oxidoreductase.	RN	[1]								
SEQUENCE FROM N.A.										
Ding B., Ryder O.A., Shi P., Zhang Y.-P.; "Molecular evolution of tyrosinase gene in primates."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.	Q9GLS0	PRELIMINARY;	PRT;	388 AA.						
EMBL; AF183681; AAG33680.1; JOINED.	ID	Q9GLS0;								
GO; GO:004503; F:monophenol monooxygenase activity; IEA.	AC	Q9GLS0;								
GO; GO:0016491; F:oxidoreductase activity; IEA.	DT	01-MAR-2001 (TREMBLrel. 16, Created)								
GO; GO:0005198; F:structural molecule activity; IEA.	DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)								
GO; GO:008152; P:metabolism; IEA.	DR	01-OCT-2003 (TREMBLrel. 25, Last annotation update)								
InterPro; IPR008922; Di-copper_centre.	DR	Tyrosinase (EC 1.14.18.1) (Fragment).								
InterPro; IPR006209; EGFR like.	DR	Trachypithecus leucocebus.								
InterPro; IPR002227; Tyrosinase.	DR	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Colobinae; Trachypithecus.								
PFam; PF00264; tyrosinase_1.	OS									
PRINTS; PR00092; TYROSINASE.	OC									
PROSITE; PS00022; EGF_1..1.	OC									
PROSITE; PS01248; LANTIN_TYPE_EGF_1..1.	OC									
Oxidoreductase.	RN	[1]								
SEQUENCE FROM N.A.										
Ding B., Ryder O.A., Shi P., Zhang Y.-P.; "Molecular evolution of tyrosinase gene in primates."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.	Q9GLS0	PRELIMINARY;	PRT;	388 AA.						
EMBL; AF183681; AAG33680.1; JOINED.	ID	Q9GLS0;								
GO; GO:004503; F:monophenol monooxygenase activity; IEA.	AC	Q9GLS0;								
GO; GO:0016491; F:oxidoreductase activity; IEA.	DT	01-MAR-2001 (TREMBLrel. 16, Created)								
GO; GO:0005198; F:structural molecule activity; IEA.	DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)								
GO; GO:008152; P:metabolism; IEA.	DR	01-OCT-2003 (TREMBLrel. 25, Last annotation update)				</td				

DR EMBL; AF183679; AAG33680..1; JOINED.  
 DR EMBL; AF183680; AAG33680..1; JOINED.  
 DR GO; GO:0044503; F:oxidoreductase activity; IEA.  
 DR GO; GO:005198; F:monophenol monooxygenase activity; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPRO08922; Di-copper\_centre.  
 DR InterPro; IPRO02049; EGFLike.  
 DR InterPro; IPRO02049; Laminin\_EGF.  
 DR InterPro; IPRO02277; Tyrosinase.  
 DR Pfam; PF00264; Tyrosinase; 1.  
 DR PRINTS; PS00092; TYROSINASE.  
 DR PROSITE; PS00022; EGF 1.; 1.  
 DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 1.  
 DR PROSITE; PS00497; TYROSINASE\_1.; 1.  
 KW Oxidoreductase.  
 FT NON\_TER 388 388 AA; 43674 MW; 5C72F3139DF344BF CRC64;  
 SQ SEQUENCE 388 AA; 43674 MW; 5C72F3139DF344BF CRC64;  
 Query Match Score 79; DB 6; Length 388;  
 Best Local Similarity 100.0%; Pred. No. 1..1e-05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 QNILLSNAPLGQQFP 15  
 Db 56 QNILLSNAPLGQQFP 70

RESULT 12  
 Q9GLS6 PRELIMINARY; PRT; 388 AA.  
 ID Q9GLS6  
 AC Q9GLS6  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Tyrosinase (EC 1.14.18.1) (Fragment).  
 OC Trachypithecus phayrei (Phayre's leaf monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Colobinae;  
 OC Trachypithecus.  
 OX NCBI\_TaxID=61618;

RN [1] SEQUENCE FROM N.A.  
 RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;  
 RT "Molecular evolution of tyrosinase gene in primates.";  
 RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF183666; AAG29587..1; -.  
 DR EMBL; AF183664; AAG29587..1; JOINED.  
 DR GO; GO:0044503; F:monophenol monooxygenase activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:005198; F:metabolism; IEA.  
 DR InterPro; IPRO08922; Di-copper\_centre.  
 DR InterPro; IPRO02049; Laminin\_EGF.  
 DR InterPro; IPRO02277; Tyrosinase.  
 DR Pfam; PF00264; Tyrosinase; 1.  
 DR PROSITE; PS00092; TYROSINASE.  
 DR PROSITE; PS00022; EGF 1.; 1.  
 DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 1.  
 DR PROSITE; PS00497; TYROSINASE\_1.; 1.  
 KW Oxidoreductase.  
 FT NON\_TER 388 388 AA; 43674 MW; 5C72F3139DF344BF CRC64;

RESULT 13  
 Q9GLS2 PRELIMINARY; PRT; 388 AA.  
 ID Q9GLS2  
 AC Q9GLS2  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Tyrosinase (EC 1.14.18.1) (Fragment).  
 OC Trachypithecus francoisi (Francois' langur) (Indochinese langur).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Colobinae;  
 OC Trachypithecus.  
 OX NCBI\_TaxID=54180;  
 RN [1] SEQUENCE FROM N.A.  
 RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;  
 RT "Molecular evolution of tyrosinase gene in primates.";  
 RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF183676; AAG33678..1; -.  
 DR EMBL; AF183674; AAG33678..1; JOINED.  
 DR EMBL; AF183675; AAG33678..1; JOINED.  
 DR GO; GO:0004513; F:monophenol monooxygenase activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR00822; Di-copper\_centre.  
 DR InterPro; IPR006209; EGF\_Like.  
 DR InterPro; IPR002449; Laminin\_EGF.  
 DR Pfam; PF00264; Tyrosinase; 1.  
 DR PROSITE; PS00022; Tyrosinase.  
 DR PROSITE; PS00249; LAMININ\_TYPE\_EGF; 1..  
 DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 1..  
 KW Oxidoreductase.  
 FT NON\_TER 388 388 AA; 43674 MW; 5C72F3139DF344BF CRC64;  
 SQ SEQUENCE 388 AA; 43674 MW; 5C72F3139DF344BF CRC64;  
 Query Match Score 79; DB 6; Length 388;  
 Best Local Similarity 100.0%; Pred. No. 1..1e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 QNILLSNAPLGQFP 15  
 Db 56 QNILLSNAPLGQFP 70

RESULT 14  
 Q9GLV4 PRELIMINARY; PRT; 388 AA.  
 ID Q9GLV4  
 AC Q9GLV4  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Tyrosinase (EC 1.14.18.1) (Fragment).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Macaca.  
 OC Cercopitheciidae; Macaca.  
 OX NCBI\_TaxID=2545;  
 RN [1] SEQUENCE FROM N.A.  
 RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;  
 RT "Molecular evolution of tyrosinase gene in primates.";  
 RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF183580; AAG26320..1; -.  
 DR EMBL; AF183578; AAG26320..1; JOINED.  
 DR GO; GO:0004503; F:monophenol monooxygenase activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR PRINTS; PR00092; TYROSINASE.  
 DR PROSITE; PS00092; EGF 1.; 1.  
 DR PROSITE; PS00022; LAMININ\_TYPE\_EGF; 1..  
 DR PROSITE; PS00497; TYROSINASE\_1.; 1.  
 KW Oxidoreductase.  
 FT NON\_TER 388 388 AA; 43674 MW; 5C72F3139DF344BF CRC64;  
 SQ SEQUENCE 388 AA; 43674 MW; 5C72F3139DF344BF CRC64;  
 Query Match Score 79; DB 6; Length 388;  
 Best Local Similarity 100.0%; Pred. No. 1..1e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR008922; Di-copper\_centre.

DR InterPro; IPR006209; Laminin\_EGF.

DR InterPro; IPR002349; Laminin\_EGF.

DR InterPro; IPR002227; Tyrosinase.

DR Pfam; PF00264; Tyrosinase; 1.

DR PRINTS; PRO0092; TYROSINASE.

DR PROSITE; PS00022; EGF 1; 1.

DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 1.

DR PROSITE; PS00497; TYROSINASE\_1; 1.

KW Oxidoreductase.

FT NON\_TER 388 SQ SEQUENCE 388 AA; 43734 MW;

5F3D551F9CFA08F CRC64;

Query Match 100.0%; Score 79; DB 6; Length 388;

Best Local Similarity 100.0%; Pred. No. 1.1e-05; Mismatches 0; Indels 0; Gaps 0;

Db 56 QNLLSNAPGPQFP 70

#### RESULT 15

Q9GT44 PRELIMINARY; PRT; 388 AA.

ID Q9GT44; AC Q9GT44;

DT 01-MAR-2001 (TREMBrel\_16; Created)

DT 01-MAR-2001 (TREMBrel\_16; Last sequence update)

DT 01-OCT-2003 (TREMBrel\_25; Last annotation update)

DE Tyrosinase (EC 1.14.18.1) (Fragment).

OS Nasalis larvatus (Proboscis monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;

OC Nasalis.

OX NCB\_TaxID=43780;

RN [1]

RP SEQUENCE FROM N.A.

RA Ding B.; Ryder O.A.; Shi P.; Zhang Y.-P.;

RT "Molecular evolution of tyrosinase gene in primates."

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF183641; AAC27276.1;

DR EMBL; AF183639; AAC27276.1; JOINED.

DR EMBL; AF183640; AAC27276.1; JOINED.

DR GO; GO:0004503; F:monophenoI monoxygenase activity; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR GO; GO:0001152; P:metabolism; IEA.

DR InterPro; IPR008922; Di-copper\_centre.

DR InterPro; IPR006209; EGF like\_-

DR InterPro; IPR02049; Laminin\_EGF.

DR InterPro; IPR02277; Tyrosinase.

DR Pfam; PF00264; Tyrosinase; 1.

DR PRINTS; PRO0092; TYROSINASE.

DR PROSITE; PS00022; EGF 1; 1.

DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 1.

DR PROSITE; PS00497; TYROSINASE\_1; 1.

KW Oxidoreductase.

FT NON\_TER 388 SQ SEQUENCE 388 AA; 43674 MW;

5C72F3139DF344BF CRC64;

Query Match 100.0%; Score 79; DB 6; Length 388;

Best Local Similarity 100.0%; Pred. No. 1.1e-05; Mismatches 0; Indels 0; Gaps 0;

Db 1 QNLLSNAPGPQFP 15

Db 56 QNLLSNAPGPQFP 70

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: June 3, 2004, 15:09:23 ; Search time 50 Seconds

(without alignments)  
84.764 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_56\_70

Perfect score: 79  
Sequence: 1 QNILLSNAPLGPQQFP 15

Scoring table: BLOSUM62

Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

- 1: GeneseqP1980s:\*
- 2: GeneseqP1990s:\*
- 3: GeneseqP2000s:\*
- 4: GeneseqP2001s:\*
- 5: GeneseqP2002s:\*
- 6: GeneseqP2003as:\*
- 7: GeneseqP2003bs:\*
- 8: GeneseqP2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	79	100.0	15	2	AAW15321	Aaw15321 Class II
2	79	100.0	15	2	AAW71591	Aaw71591 Class II
3	79	100.0	15	2	AAW85296	Aaw85296 Helper T-
4	79	100.0	15	2	AYY40209	Aay40209 Amino aci
5	79	100.0	15	2	AYY33168	Aay33168 Human tyr
6	79	100.0	15	2	AYY26865	Aay26865 Melanoma-
7	79	100.0	15	2	AYY00710	Aay00710 Tumour an
8	79	100.0	15	2	AYY49658	Aay49658 Tumour an
9	79	100.0	15	2	AYY01748	Aay01748 Exemplary
10	79	100.0	15	3	AYY71515	Aay71515 Human Tyr
11	79	100.0	15	3	AAB13739	Aab13739 Peptide f
12	79	100.0	15	3	AYY92295	Aay92295 Tyrosinas
13	79	100.0	15	3	AYY84291	Aay84291 Tumour as
14	79	100.0	15	3	AYY82974	Aay82974 Tyrosinas
15	79	100.0	15	3	ABO02617	Aab02617 Tumour as
16	79	100.0	15	3	ABO08689	Aab08689 Antigenic
17	79	100.0	15	4	AMN9392	Aamn9392 Vaccine r
18	79	100.0	15	4	AAB02106	Aae02106 Tyrosinas
19	79	100.0	15	4	AAB31349	Aab31349 Exemplary
20	79	100.0	15	4	AAB06836	Aae06836 Human tyr
21	79	100.0	15	5	ABG79139	Abg79139 Human Tyr
22	79	100.0	15	5	ADA19078	Aae19078 HLA-DR4 r
23	79	100.0	15	6	ADA19543	Ada19543 Human can
24	79	100.0	30	5	AAB84892	Aau84892 Human Tyr
25	79	100.0	273	2	AR48358	Aar48358 Human tyr

## ALIGNMENTS

RESULT 1	AAW15321	ID	AAW15321 standard; peptide; 15 AA.
	XX	AC	AAW15321;
	XX	DT	09-FEB-1998 (first entry)
	XX	DE	Class II restricted melanoma tyrosinase derived antigenic peptide 1.
	XX	XX	Major histocompatibility complex; MHC; Class II; tyrosinase; vaccine; immune response; immunogenic peptide; melanoma; treatment; protective antibody; immune cells; CD8+ T cell; CD4+ T cell.
	XX	XX	Synthetic.
	OS	OS	Homo sapiens.
	XX	PN	W09711669-A2.
	XX	PD	03-APR-1997.
	XX	PP	25-SEP-1996; 96WO-US015346.
	XX	PR	26-SEP-1995; 95US-00533895.
	PA	(USSH ) US DEBT HEALTH & HUMAN SERVICES.	
	XX	PI	Topalian SL, Rosenberg SA, Robbins PF.
	XX	XX	WPI; 1997-212652/19.
	XX	PT	Major histocompatibility complex Class H immunogenic peptide - used to prevent or treat melanoma in mammal by stimulating production of protective antibodies or immune cells.
	XX	Claim 2; Page 59;	79pp; English.
	CC	Peptides AAW15321-56 are major histocompatibility complex (MHC) Class II restricted melanoma peptides, derived from tyrosinase. Tumour reactive T cells recognise melanoma antigens encoded by the tyrosinase gene. The present sequence is derived from amino acids 56-70. The peptides may be used as a vaccine, either prophylactically in advance of any evidence of melanoma, or therapeutically to enhance the patients own immune response. The immunogenic peptides can be used to prevent or treat melanoma in a mammal by stimulating the production of protective antibodies or immune cells, preferably immune positive CD4+ T cells	
	CC	Sequence 15 AA;	



Db 1 QNILLSNAPLGQFP 15

RESULT 4  
AY40209 ID AAY40209 standard; peptide; 15 AA.  
XX AC AAY40209;  
AC AAY40209;

DT 19-NOV-1999 (first entry)  
XX Amino acid sequence of a human melanoma epitope.  
XX Cytotoxic T cell; T lymphocyte; CD8+ epitope; T helper cell;  
KW CD4+ epitope; B epitope; lipopeptide; interferon gamma; adjuvant;  
KW vaccine; tumor; infection; immune response; cytokine profile;  
KW acquired immune deficiency syndrome; papilloma; cancer; hepatitis;  
KW autoimmune disease.  
OS Homo sapiens.  
XX PN FR2774687-A1.  
XX PD 13-AUG-1999.  
XX PP 06-FEB-1998; 98FR-00001439.  
XX PR 06-FEB-1998; 98FR-00001439.  
XX PA (INERM ) INSERM NAT SANTE & RECH MEDICALE.  
PA (INSP ) INST PASTEUR LILLE.  
XX PI Thiam K, Guillet JG, Ver Waerde C, Auriault C, Gras MH, Loing E;  
XX DR WPI; 1999-510734/43.

PT New lipopeptide comprising C-terminal interferon-gamma fragment with  
PT attached lipophilic groups, used as interferon mimic, e.g. for treating  
PT cancer or virus infection.  
XX Disclosure; Page 35; 54PP; French.  
PS AAY40123-Y40379 represent epitopes that are able to activate cytotoxic T  
CC lymphocytes (CD8+ epitopes), T helper cells (CD4+ epitopes), or B  
CC epitopes recognized by corresponding antibodies. The epitopes may be used  
CC in the composition of the invention. The specification describes a  
CC lipopeptide that has a peptide part derived from mammalian interferon  
CC gamma (IFNG), and one or more lipophilic parts comprising a linear or  
CC branched, (un)saturated 4-20C hydrocarbon chain or a steroid. The  
CC lipopeptide mimics the activity of IFNG. Compositions comprising the  
CC lipopeptides are used to treat or prevent any condition that responds to  
CC IFNG, and as adjuvant for vaccines (particularly those directed against  
CC tumors, viral or parasitic infections), to stimulate or (re)orient the  
CC immune response between types 1 and 2 cytokine profiles. Particular  
CC applications are treatment of infections (particularly viral, e.g.  
CC acquired immune deficiency syndrome, papilloma (cancer) and hepatitis,  
CC but also bacterial, fungal, parasitic or helminth); cancers (particularly  
CC of kidney, cutaneous T cells or ovary, chronic myelogenous leukemia or  
CC mesothelioma), allergy; and autoimmune diseases

SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAY33168  
ID AAY33168 standard; peptide; 15 AA.  
XX AC AAY33168;  
XX DT 17-NOV-1999 (first entry)  
XX DE Human tyrosinase peptide #7.  
XX KW Human; protein delivery; Yersinia sp; effector gene; mutant; antigen;  
KW immune response; cytotoxic T-lymphocyte; CTL; vaccination; treatment;  
KW pathological disorder; tyrosinase.  
XX OS Homo sapiens.  
XX PN WO945098-A2.  
XX PD 10-SEP-1999.  
XX PF 03-MAR-1999; 99WO-IB000587.  
XX PR 06-MAR-1998; 98US-00036532.  
XX PA (VBRU/) VAN DER BRUGGEN P. B.  
PA (CORN/) CORNLIS G. R.  
PA (BOLA/) BOLAND A. M.  
PA (BOON/) BOON-PALLEUR T. R.  
XX PT Van Der Bruggen PB, Cornelis GR, Boland AM, Boon-Palleur TR;  
XX WPI; 1999-540840/45.  
XX PT New mutant Yersinia strains useful for treating a pathological disorder.  
XX Example 1 ; Page 70; 80pp; English.  
XX CC This invention describes a novel mutant Yersinia (Y1) strain, comprising  
CC mutation(s) in effector-encoding gene(s) and deficient in the production  
CC of functional effector protein(s). The invention describes (1) a  
CC quintuple mutant Yersinia strain, having the designation Yersinia  
CC enterocolitica yopHEMP or Yersinia Pseudotuberculosis yopHEAO; (2) an  
CC expression vector (EVL) for delivering a heterologous protein into a  
CC mutant Yersinia strain for delivering a heterologous protein into a  
CC eukaryotic cell, comprising contacting the cell with a Y1 transformed  
CC with the above vector (Y1-EV1); (4) a method for delivering a  
CC heterologous protein into a eukaryotic cell, comprising contacting the  
CC cell with a Y1 transformed with the above vector (Y1-EV1); (5) a method  
CC for inducing an immune response specific for a heterologous protein; (6)  
CC a method for inducing a cytotoxic T-lymphocyte (CTL) response specific  
CC for a heterologous protein; (7) a method for determining the efficacy of  
CC an antigen vaccination regimen in a subject. Y1 is used to treat a  
CC pathological disorder, by providing recombinant Yersinia for the safe  
CC delivery of proteins into eukaryotic cells. AAY33147-Y33178 are human-  
CC derived peptides used to illustrate the method of the invention  
XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFP 15  
DB 1 QNILLSNAPLGQFP 15

RESULT 6  
AY26865  
ID AAY26865 standard; peptide; 15 AA.  
XX AC AAY26865;  
XX

RESULT 5

DT	14-SEP-1999	(first entry)	PN	WO9858956-A2.
XX	DE	Melanoma-derived lipopeptide epitope #6 for mixed micelles.	XX	30-DEC-1998.
XX	DE	Micelle; microaggregate; induction; immune response; lipopeptide; CTL;	PD	
KW	XX	cytotoxic T-lymphocyte; epitope; lipid; helper T-lymphocyte; HTL; HBV;	XX	19-JUN-1998;
KW	XX	tetanus; toxin; vaccine; HIV; hepatitis B virus; papilloma virus; p53;	PF	98WO-US012894.
KW	XX	Plasmodium falciparum; malaria.	XX	23-JUN-1997;
XX	PA	(LUDWIG INST CANCER RES.	PR	97US-00880979.
OS	PI	XII	PA	
OS	PI	Warnier G, Uyttenhove C, Boon-Falleur T;	XX	
Homo sapiens.	PI		XX	
XX	PR	Immunization methods using viruses expressing antigen for priming and	XX	
XX	PR	booster immunizations - useful for modulating immune responses against	XX	
XX	PR	antigen, e.g. enhancing immune response against tumour cells expressing	XX	
XX	PR	tumour rejection antigens.	XX	
PS	Disclosure:	Page 9 ; 33pp; English.	XX	
PA	CC	This sequence represents a tumour antigen booster peptide that can be	XX	
PA	CC	used in the method of the invention. The method is for for modulating an	CC	
(CNRS ) CNRS CENT NAT RECH SCI.	CC	immune response in a mammal against an antigen, and comprises: (A)	CC	
(INSP ) INST PASTEUR LILLE.	CC	inducing an immune response by: (i) administering a virus containing a	CC	
XX	CC	nucleic acid molecule encoding the antigen or its precursor to generate	CC	
XX	CC	an immune response; and (ii) administering at least one booster dose	CC	
XX	CC	comprising a peptide including the antigen, in an adjuvant, in a combined	CC	
PA	CC	amount effective to enhance the initial immune response; or (B) reducing	CC	
PA	CC	an immune response as defined for (A) but using a non-adjuvant with the	CC	
(INSP ) INST PASTEUR LILLE.	CC	peptide which includes the antigen, in an amount effective to reduce the	CC	
XX	CC	initial immune response. Method (A) is used to enhance the immune	CC	
XX	CC	response against tumour cells expressing tumour rejection antigens, and	CC	
XX	CC	against pathogens in subjects having human leukocyte antigen-presenting	CC	
XX	CC	molecules. Method (B) is used to reduce the immune response in allergy,	CC	
XX	CC	autoimmune disease, and allograft rejection. Method (A) provides an	CC	
XX	CC	immunization method which, unlike prior art, is not limited by the host	CC	
XX	CC	immune response against viral vectors	XX	
XX	SQ	Sequence 15 AA;	XX	
XX	Query Match	Score 79; DB 2; Length 15;	Query	1 QNILLSNAPLGQPQP 15
XX	Best Local Similarity	Pred. No. 1.2e-06;	Best Local Similarity	100.0%; Pred. No. 1.2e-06;
XX	Matches	Indels 0;	Matches	0; Mismatches 0; Indels 0;
XX	XX	Gaps 0;	XX	Gaps 0;
XX	XX	Sequence 15 AA;	XX	
XX	Query Match	Score 79; DB 2; Length 15;	RESULT 8	AY49658
XX	Best Local Similarity	Pred. No. 1.2e-06;	ID	AY49658 standard; peptide; 15 AA.
XX	Matches	Indels 0;	XX	
XX	XX	Gaps 0;	AC	
XX	XX	Sequence 15 AA;	AC	
XX	XX	Query Match	AY49658;	
XX	XX	Best Local Similarity	AY49658	
XX	XX	Matches	AY49658;	
XX	XX	Indels 0;	DT	14-JAN-2000 (first entry)
XX	XX	Gaps 0;	DE	Tumour antigenic peptide SEQ ID NO:25.
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	
XX	XX	Gaps 0;	XX	
XX	XX	Sequence 15 AA;	XX	
XX	XX	Query Match	XX	
XX	XX	Best Local Similarity	XX	
XX	XX	Matches	XX	
XX	XX	Indels 0;	XX	



histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte Antigen), that are recognised by T-lymphocytes and elicit an immune response from cytotoxic T-lymphocytes (CTL). They function as an immune response stimulator. Tumour rejection antigens are useful in prophylaxis, therapy and diagnosis of tumours and are effective in controlling or preventing tumour growth. The present sequence is the human Tyrosinase peptide-5, that corresponds to residues 56-70 of the tumour associated gene, tyrosinase encoding protein. It can be administered to induce or enhance an immune response and is presented by HLA-DR4 complex. This peptide can serve as a tumour rejection antigen (TRA) and in combination with adjuvants, can produce vaccines useful for treating a variety of tumours.

Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 QNILLSNAPLGQFP 15

Qy 1 QNILLSNAPLGQFP 15

RESULT 11  
AAB13739 standard; peptide; 15 AA.ID AAB13739  
XX AC  
XX DT 02-FEB-2001 (first entry)

XX DE Peptide fragment # 5 from human tyrosinase.

XX XX Human; T-cell; immune response; antigen; B7 family molecule;

XX Leukocyte function-associated antigen-3; LFA-3;

XX Intercellular adhesion molecule-1; ICAM-1; vaccine; immunotherapy;

XX Colon polyp; Crohn's disease; ulcerative colitis; breast lesion; tumour;

XX tyrosinase.

XX Homo sapiens.

OS XX WO200034494-A1.

PN XX PD 15-JUN-2000.

XX PF 12-NOV-1999; 99WO-US026866.

XX PR 09-DEC-1998; 98US-0111582P.

XX PA (USSH ) US DEPT HEALTH &amp; HUMAN SERVICES.

PA (THER-) THERION BIOLGICS CORP.

PA Schlom J, Hodge J, Panicali D;

XX DR 2000-431307/37.

PS Claim 18; Page 35; 188pp; English.

XX Costimulatory molecules have important roles in T-cell activation and therefore the immune response. The present invention relates to recombinant vectors which comprise of costimulatory molecules: a B7 family molecule,

CC encoding at least three costimulatory molecules: a B7 family molecule,

CC Leukocyte function-associated antigen-3 (LFA-3, human CD58) and

CC Intercellular adhesion molecule-1 (ICAM-1, CD54) and optionally a foreign

CC gene encoding a target antigen or immunological epitope. The present

CC sequence is one such target antigen used in the present invention. The

CC present sequence is a tumour-associated antigen. The vector of the

CC

present invention would be useful for providing an enhanced immune response to the present target antigen. The vector of the present invention may therefore be useful in immunotherapy for treating or preventing diseases caused by viruses, bacteria, protozoans, parasites, pre-malignant cells and tumour cells. The recombinant vector can be used to treat or prevent preneoplastic or hyperplastic states such as colon polyps, Crohn's disease, ulcerative colitis and breast lesions.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 QNILLSNAPLGQFP 15

Qy 1 QNILLSNAPLGQFP 15

RESULT 12  
AAY92295 standard; peptide; 15 AA.ID AAY92295  
XX AC  
XX DT 10-AUG-2000 (first entry)

XX DE Tyrosinase antigenic peptide epitope (residues 56-70).

XX KW Tyrosinase; antigen; epitope; cytotoxic T lymphocyte; CTL; complex;

XX human leukocyte antigen; HLA.

XX Homo sapiens.

OS XX PN WO200020445-A2.

XX PD 13-APR-2000.

XX PP 15-SEP-1999; 99WO-1B001664.

XX XX PR 02-OCT-1998; 98US-00165163.

XX PR 03-APR-1999; 99US-00289350.

XX PA (CHAU /) CHAUX P.

PA (LUTT /) LUTTEN R.

PA (DEMO /) DEMOTTE N.

PA (DUFFY /) DUFFOUR M.

PA (LURQ /) LURQUIN C.

PA (TRAV /) TRAVERSARI C.

PA (STRO /) STROOBANT V.

PA (CORN /) CORNELIS G.R.

PA (BOON /) BOON-FALLIER T.

PA (VBRU /) VAN DER BRUGGEN P.

PA (SCHU /) SCHULTZ E.

PA (WARN /) WARNIER G.

XX PT Isolation of cytotoxic T-lymphocytes clones by successive steps of

PT stimulation and testing of lymphocytes with antigen presenting cells

PT which present antigens derived from different expression systems

PT Disclosure; Page 22; 99pp; English.

XX PI Stroobant V, Cornelis GR, Boon-Fallier T, Van der Bruggen P;

PI Schultz E, Warnier G;

XX DR WPI; 2000-303739/26.

XX PT Isolation of cytotoxic T-lymphocytes clones by successive steps of

PT stimulation and testing of lymphocytes with antigen presenting cells

PT which present antigens derived from different expression systems

PT Disclosure; Page 22; 99pp; English.

XX PI Chaux P, Lutten R, Demotte N, Duffour M, Lurquin C, Traversari C;

PI Stroobant V, Cornelis GR, Boon-Fallier T, Van der Bruggen P;

PI Schultz E, Warnier G;

XX DR WPI; 2000-303739/26.

XX PT Isolation of cytotoxic T-lymphocytes (CTL) clones

PT which present antigens derived from different expression systems

PT Disclosure; Page 22; 99pp; English.

XX A novel method of isolation of cytotoxic T-lymphocytes with

CC antigen presenting cells (APCs) which present antigens derived from

CC different expression systems. The CTL clones isolated recognize specific

CC antigenic peptides of proteins, preferably of the MAGE family. The APC is

CC

autologous and each expression systems is different from at least one of the other expression systems, therefore isolating a cytotoxic T cell clone specific for the protein. The method can also be used to identify an antigenic peptide epitope. Isolated CTL clones specific for a peptide/human leukocyte antigen (HLA) complex are claimed. The CTL cells specific for the complexes, peptides or cells which present the complexes on the cell surface are useful for treating pathological conditions characterized by abnormal expression of the complexes.

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
ID AAY84291 standard; peptide; 15 AA.  
XX  
AC AAY84291;  
XX DT 12-JUL-2000 (first entry)  
XX DB Tumour associated antigen derived from tyrosinase.  
XX KW tumour rejection antigen; macrophage colony stimulating gene;  
KW macrophage-colony stimulating factor; antigen presenting cell;  
KW human leucocyte antigen; CD8+ cytotoxic T lymphocyte.  
XX OS Homo sapiens.  
XX PN WO20001369-A1.  
XX PD 16-MAR-2000.  
XX PR 03-SEP-1999; 99WO-US020344.  
XX PR 04-SEP-1998; 98US-0099077P.  
XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Probst-Keppler M, Van Den Eynde B, Boon-Falleur T;  
XX DR 2000-256859/22.  
PT Isolated polypeptide used to treat subjects having a disorder characterized by expression of alternative open reading frame macrophage-colony stimulating factor comprises 25 amino acid residue sequence.  
XX Disclosure; Page 20; 74pp; English.  
XX AAY84270-184303 represent peptides which are tumour associated antigens. They can be administered in conjunction with the tumour rejection antigen precursor of the invention to induce anti-tumour responses. The tumour rejection antigen precursor of the invention is encoded by an alternative open reading frame (ORF) of human macrophage colony stimulating gene. Peptides derived from the alternative ORF of macrophage-colony stimulating factor, when presented by an antigen presenting cell having a human leucocyte antigen (HLA) class I molecule, effectively induce the activation and proliferation of CD8+ cytotoxic T lymphocytes. Polypeptide and nucleic acids derived from the alternate ORF of macrophage-colony stimulating factor are useful for enriching selectively a population of T lymphocytes with CD8+ T lymphocytes. They are also useful for diagnosing a disorder characterized by expression of the polypeptide, and for identifying functional variants and mimetics

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

CC the other expression systems, therefore isolating a cytotoxic T cell

CC clone specific for the protein. The method can also be used to identify

CC an antigenic peptide epitope. Isolated CTL clones specific for a

CC peptide/human leukocyte antigen (HLA) complex are claimed. The CTL cells

CC specific for the complexes, peptides or cells which present the complexes

CC on the cell surface are useful for treating pathological conditions

CC characterized by abnormal expression of the complexes.

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Prd. No. 1.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Sq 1 QNTILSNAPLGQFP 15  
 Db 1 QNTILSNAPLGQFP 15  
 1 QNTILSNAPLGQFP 15

## RESULT 15

AAB02617

ID AAB02617 standard; peptide; 15 AA.

XX

AC AAB02617;

XX

DT 18-AUG-2000 (first entry)

XX

DE Tumour associated peptide antigen from Tyrosinase #6.

XX

XX MAGE-A3; HLA class II; human leukocyte antigen; antibody; vaccine;  
 KW cancer; human; tumour; tumour associated gene product.

XX

OS Homo sapiens.

XX

PN WO2000020581-A1.

XX

PD 13-APR-2000.

XX

PF 15-SEP-1999; 99WO-US021230.

XX

PR 05-OCT-1998; 98US-00166448.

XX

PA (LUDWIG INST CANCER RES.  
 PA (UYVR-) UNIV VRIJE BRUSSEL.

XX

PI Chaux P, Stroobant V, Boon-Falleur T, Van Der Bruggen P,  
 PI Schultz ES, Van Snick J, Lete B, Thielemans K, Corthals J;  
 PI Heirman C;

XX

DR WPI; 2000-317713/27.

XX

PT New MAGE-A3 class II binding peptides, useful to diagnose and treat  
 PT tumors, are fragments of MAGE-A3 which bind to and are presented to T  
 PT lymphocytes by human leukocyte antigen class II molecules.

XX

PS Disclosure; Page 33; 119PP; English.

XX

CC The present invention relates to MAGE-A3 (tumour associated gene product)  
 CC human leukocyte antigen (HLA) class II-binding peptides (see AAB02566-  
 CC B02595, and AAB02633-B02637). These peptides are presented to T cells in  
 CC the context of HLA class II molecules. The peptides stimulate the  
 CC activity and proliferation of CD4+ T lymphocytes. The invention also  
 CC includes nucleotide sequences encoding MAGE-A3 peptides (see AAA37928 and  
 CC AAA37938-A37940). The peptides and nucleotide sequences can be used to  
 CC create antibodies against the MAGE-A3 peptides. The antibodies, peptides  
 CC and nucleotide sequences can be used to create a vaccine. The peptides  
 CC are used to diagnose or treat a disorder characterized by expression of  
 CC MAGE-3, particularly cancer. The methods can also be used in the  
 CC diagnosis of disorders associated with MAGE-3 expression. Included in the  
 CC invention are other human tumour antigens (see AAB02596-B02637), and PCR  
 CC primers used in the course of the invention (see AAA37929-A37937 and  
 CC AAA37941-A37942).

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Sq 1 QNTILSNAPLGQFP 15  
 Db 1 QNTILSNAPLGQFP 15

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## OM protein - protein search, using sw mode!

Run on: June 3, 2004, 15:14:49 ; Search time 39 Seconds  
 (without alignments)  
 1.08.207 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_56\_70  
 Perfect score: 79  
 Sequence: 1 QNLLSNAPLGQQFP 15

Scoring table: BLOSUM62

Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%

Maximum Match 100%

Listing first 45 summaries

Published Applications AA:  
 1: /cgm2\_6\_ptodata/1/pubpa/us07\_pubcomb.pep:  
 2: /cgm2\_6\_ptodata/1/pubpa/us07\_pubcomb.pep:  
 3: /cgm2\_6\_ptodata/1/pubpa/us06\_pub\_comb.pep:  
 4: /cgm2\_6\_ptodata/1/pubpa/us06\_pubcomb.pep:  
 5: /cgm2\_6\_ptodata/1/pubpa/us07\_new\_pub\_pep:  
 6: /cgm2\_6\_ptodata/1/pubpa/pctus\_pubcomb.pep:  
 7: /cgm2\_6\_ptodata/1/pubpa/us08\_new\_pub\_pep:  
 8: /cgm2\_6\_ptodata/1/pubpa/us08\_pubcomb.pep:  
 9: /cgm2\_6\_ptodata/1/pubpa/us09\_pubcomb.pep:  
 10: /cgm2\_6\_ptodata/1/pubpa/us09\_pubcomb.pep:  
 11: /cgm2\_6\_ptodata/1/pubpa/us09\_pubcomb.pep:  
 12: /cgm2\_6\_ptodata/1/pubpa/us09\_new\_pub\_pep:  
 13: /cgm2\_6\_ptodata/1/pubpa/us09\_pubcomb.pep:  
 14: /cgm2\_6\_ptodata/1/pubpa/us08\_pubcomb.pep:  
 15: /cgm2\_6\_ptodata/1/pubpa/us08\_pubcomb.pep:  
 16: /cgm2\_6\_ptodata/1/pubpa/us09\_new\_pub\_pep:  
 17: /cgm2\_6\_ptodata/1/pubpa/us60\_new\_pub\_pep:  
 18: /cgm2\_6\_ptodata/1/pubpa/us60\_pubcomb.pep:  
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	15	9 US-09-923-821-25	Sequence 25, Appl
2	79	100.0	15	9 US-09-923-821-37	Sequence 37, Appl
3	79	100.0	15	12 US-10-218-995-32	Sequence 32, Appl
4	79	100.0	15	12 US-10-253-286-500	Sequence 500, App
5	79	100.0	15	12 US-10-103-995-198	Sequence 198, Appl
6	79	100.0	15	14 US-10-161-997-24	Sequence 24, Appl
7	79	100.0	15	14 US-10-170-932-66	Sequence 66, Appl
8	79	100.0	15	14 US-10-239-313A-95	Sequence 495, App
9	79	100.0	15	15 US-10-245-971-500	Sequence 500, App
10	79	100.0	15	15 US-10-406-217-13	Sequence 13, Appl
11	79	100.0	15	16 US-10-297-68-13	Sequence 13, Appl
12	79	100.0	20	12 US-10-253-286-503	Sequence 503, App
13	79	100.0	20	15 US-10-245-971-503	Sequence 503, App
14	79	100.0	30	12 US-10-296-334-978	Sequence 978, App
15	79	100.0	32	12 US-10-253-286-525	Sequence 525, App

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	15	9 US-09-923-821-25	Sequence 25, Appl
2	79	100.0	15	9 US-09-923-821-37	Sequence 37, Appl
3	79	100.0	15	12 US-10-218-995-32	Sequence 32, Appl
4	79	100.0	15	12 US-10-253-286-500	Sequence 500, App
5	79	100.0	15	12 US-10-103-995-198	Sequence 198, Appl
6	79	100.0	15	14 US-10-161-997-24	Sequence 24, Appl
7	79	100.0	15	14 US-10-170-932-66	Sequence 66, Appl
8	79	100.0	15	14 US-10-239-313A-95	Sequence 495, App
9	79	100.0	15	15 US-10-245-971-500	Sequence 500, App
10	79	100.0	15	15 US-10-406-217-13	Sequence 13, Appl
11	79	100.0	15	16 US-10-297-68-13	Sequence 13, Appl
12	79	100.0	20	12 US-10-253-286-503	Sequence 503, App
13	79	100.0	20	15 US-10-245-971-503	Sequence 503, App
14	79	100.0	30	12 US-10-296-334-978	Sequence 978, App
15	79	100.0	32	12 US-10-253-286-525	Sequence 525, App

RESULT 1  
 US-09-923-831-25  
 / Sequence 25, Application US/09923831

GENERAL INFORMATION:  
 / APPLICANT: Martelange, Valérie  
 / PATENT NO. US20020117142A1  
 / TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
 / FILE REFERENCE: L0461/7054  
 / CURRENT APPLICATION NUMBER: US/09-923, 831  
 / CURRENT FILING DATE: 2001-08-07  
 / PRIOR APPLICATION NUMBER: 09-183, 706  
 / PRIOR FILING DATE: 2001-10-30  
 / NUMBER OF SEQ ID NOS: 43  
 / SEQ ID NO: 25  
 / LENGTH: 15  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 US-09-923-831-25

RESULT 2  
 US-09-766-889A-37  
 / Sequence 37, Application US/09766889A  
 / PATENT NO. US20030161654A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Luiten, Rosalie  
 / APPLICANT: Boon-Faileur, Thierry  
 / APPLICANT: van der Bruggen, Pierre

APPLICANT: Stroobant, Vincent  
 APPLICANT: Demotte, Nathalie  
 APPLICANT: Schultz, Erwin  
 TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44  
 FILE REFERENCE: L0461/7104  
 CURRENT APPLICATION NUMBER: US/09/766, 889A  
 CURRENT FILING DATE: 2001-01-19  
 PRIOR APPLICATION NUMBER: US 60/177, 242  
 PRIOR FILING DATE: 2000-01-20  
 PRIOR APPLICATION NUMBER: US 60/243, 212  
 PRIOR FILING DATE: 2000-10-25  
 NUMBER OF SEQ ID NOS: 59  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 37  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-766-889A-37

Query Match 100.0%; Score 79; DB 9; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
 Db 1 QNILLSNAPLGQQFP 15

---

RESULT 3  
 US-10-218-095-32  
 Sequence 32, Application US/10218095  
 Publication No. US20040033541A1  
 GENERAL INFORMATION:  
 APPLICANT: Zhang, Yi  
 APPLICANT: Stroobant, Vincent  
 APPLICANT: Russo, Vincenzo  
 APPLICANT: Boon-Falleur, Thierry  
 APPLICANT: van der Bruggen, Pierre  
 TITLE OF INVENTION: MAGP-A4 ANTIGENIC PEPTIDES AND USES THEREOF  
 FILE REFERENCE: L0461/70137  
 CURRENT APPLICATION NUMBER: US/10/218, 095  
 CURRENT FILING DATE: 2002-08-13  
 NUMBER OF SEQ ID NOS: 63  
 SOFTWARE: Patentin version 3.1  
 SEQ ID NO: 32  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-218-095-32

Query Match 100.0%; Score 79; DB 12; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
 Db 1 QNILLSNAPLGQQFP 15

---

RESULT 4  
 US-10-253-286-500  
 Sequence 500, Application US/10253286  
 Publication No. US20040054881A1  
 GENERAL INFORMATION:  
 APPLICANT: HUMPHREYS, ROBERT  
 APPLICANT: XU, MINZHEN  
 TITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
 FILE REFERENCE: REH-2015  
 CURRENT APPLICATION NUMBER: US/10/253, 286  
 CURRENT FILING DATE: 2003-01-13  
 PRIOR APPLICATION NUMBER: 10/197, 000  
 PRIOR FILING DATE: 2002-07-17  
 PRIOR APPLICATION NUMBER: 09/396, 813

Query Match 100.0%; Score 79; DB 12; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
 Db 1 QNILLSNAPLGQQFP 15

---

RESULT 5  
 US-10-103-395-198  
 Sequence 198, Application US/10103395  
 Publication No. US20020160019A1  
 GENERAL INFORMATION:  
 APPLICANT: EPIMUNE, Inc.  
 APPLICANT: Sette, Alessandro  
 APPLICANT: Sidney, John  
 APPLICANT: Southwood, Scott  
 TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR  
 TITLE OF INVENTION: RESTRICTED EPITOPIES  
 FILE REFERENCE: 39963-20016-01  
 CURRENT APPLICATION NUMBER: US/10/103, 395  
 PRIOR APPLICATION NUMBER: US/09/009, 953  
 PRIOR FILING DATE: 2003-01-03  
 PRIOR APPLICATION NUMBER: PCT/US98/01373  
 PRIOR FILING DATE: 1998-01-21  
 PRIOR APPLICATION NUMBER: US/09/036, 713  
 PRIOR FILING DATE: 1997-01-23  
 PRIOR APPLICATION NUMBER: US/09/037, 432  
 PRIOR FILING DATE: 1997-01-07  
 NUMBER OF SEQ ID NOS: 274  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 198  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-103-395-198

Query Match 100.0%; Score 79; DB 12; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
 Db 1 QNILLSNAPLGQQFP 15

---

RESULT 6  
 US-10-161-097-24  
 Sequence 24, Application US/10161097  
 Publication No. US20030096404A1  
 GENERAL INFORMATION:  
 APPLICANT: ROSENZWEIG, Michael C.  
 APPLICANT: PYKET, Mark J.  
 APPLICANT: SCADDEN, David T.  
 APPLICANT: POZNANSKY, Mark C.  
 TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION  
 TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL  
 TITLE OF INVENTION: DEVICES  
 FILE REFERENCE: C1005/7012/XA/ERG  
 CURRENT APPLICATION NUMBER: US/10/161, 097  
 CURRENT FILING DATE: 2002-05-31  
 PRIOR APPLICATION NUMBER: US/09/574, 749

PRIOR FILING DATE: 2002-05-31  
; PRIOR APPLICATION NUMBER: US 60/107,972  
; PRIORITY FILING DATE: 1998-11-12  
; PRIORITY APPLICATION NUMBER: PCT/US99/26795  
; PRIORITY FILING DATE: 1999-11-12  
; PRIORITY APPLICATION NUMBER: US 09/524,749  
; PRIORITY FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO: 24  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Homo Sapiens source  
; US-10-161-097-24

Query Match Score 79; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

RESULT 7  
US-10-170-832-66  
; Sequence 66, Application US/101/0832  
; Publication No. US20030170792A1  
; GENERAL INFORMATION:  
; APPLICANT: Chaux, Paschal  
; APPLICANT: Vantcomme, Valrie  
; APPLICANT: Stroobant, Vincent  
; APPLICANT: Boon-Faillour, Thierry  
; APPLICANT: van der Bruggen, Pierre  
; APPLICANT: Thielemans, Kris  
; APPLICANT: Corthals, Jurgen  
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
; FILE REFERENCE: L04617052  
; CURRENT FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: US/09/166,448  
; PRIORITY FILING DATE: 1998-10-05  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO: 66  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; US-10-170-832-66

Query Match Score 79; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

RESULT 8  
US-10-239-313A-495  
; Sequence 495, Application US/10239313A  
; Publication No. US2003175285A1  
; GENERAL INFORMATION:  
; APPLICANT: KLINGNER - HAMOUR, Christine  
; APPLICANT: CORVIA, Nathalie  
; APPLICANT: BECK, Alain  
; APPLICANT: GOETSCHE, Liliane  
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID  
; TITLE OF INVENTION:

FILE REFERENCE: 343 727 - US  
; CURRENT APPLICATION NUMBER: US/10/239,313A  
; CURRENT FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: FR 00/03711  
; PRIORITY FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: PCT 01/70772  
; NUMBER OF SEQ ID NOS: 697  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 495  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-239-313A-495

Query Match Score 79; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

RESULT 9  
US-10-245-871-500  
; Sequence 500, Application US/10245871  
; Publication No. US2003023594A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: REH-2013  
; CURRENT APPLICATION NUMBER: US/10/245,871  
; CURRENT FILING DATE: 2003-01-09  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 09/396,813  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 905  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 500  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; US-10-245-871-500

Query Match Score 79; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
Db 1 QNILLSNAPLGQQFP 15

RESULT 10  
US-10-406-317-13  
; Sequence 13, Application US/10406317  
; Publication No. US20040019195A1  
; GENERAL INFORMATION:  
; APPLICANT: Panicali, Dennis  
; APPLICANT: Hodge, James  
; APPLICANT: Hodge, Jeffrey  
; APPLICANT: Panicali, Dennis  
; TITLE OF INVENTION: A recombinant vector expressing multiple constimulatory molecules and uses thereof  
; FILE REFERENCE: 38-63-0189  
; CURRENT APPLICATION NUMBER: US/10/406,317  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US/09/856,988  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: PCT/US99/26866  
; PRIOR FILING DATE: 1999-11-12

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; PRIOR APPLICATION NUMBER: 60/111,582
; PRIOR FILING DATE: 1998-12-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-10-406-317-13

Query Match          100.0%; Score 79; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e-06; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; DB 15; Length 20;
Qy      1 QNILLSNAPLGQFP 15
Db      1 QNILLSNAPLGQFP 15

RESULT 11
US-10-297-168-13
; Sequence 13, Application US/10297168
; Publication No. US20040091995A1
; GENERAL INFORMATION:
; APPLICANT: SCHLOM, Jeffrey
; APPLICANT: GREINER, John W.
; APPLICANT: KASS, Erik
; APPLICANT: PANICAI, Dennis
; TITLE OF INVENTION: RECOMBINANT NON-REPLICATING VIRUS EXPRESSING GM-CSF AND
; TITLE OF INVENTION: USES THEREOF TO ENHANCE IMMUNE RESPONSES
; FILE REFERENCE: 3B13-0167
; CURRENT APPLICATION NUMBER: US/10/297,168
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: PCT/US01/19201
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US60/211,717
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-297-168-13

Query Match          100.0%; Score 79; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e-06; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; DB 16; Length 20;
Qy      1 QNILLSNAPLGQFP 15
Db      1 QNILLSNAPLGQFP 15

RESULT 12
US-10-253-286-503
; Sequence 503, Application US/10253286
; Publication No. US20040054881A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2015
; CURRENT APPLICATION NUMBER: US/10/253,286
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 503
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-10-253-286-503

Query Match          100.0%; Score 79; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.3e-06; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; DB 15; Length 20;
Qy      1 QNILLSNAPLGQFP 15
Db      6 QNILLSNAPLGQFP 20

RESULT 13
US-10-245-071-503
; Sequence 503, Application US/10245871
; Publication No. US20030235594A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2013
; CURRENT APPLICATION NUMBER: US/10/245,871
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 503
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-10-245-071-503

Query Match          100.0%; Score 79; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.3e-06; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; DB 15; Length 20;
Qy      1 QNILLSNAPLGQFP 15
Db      6 QNILLSNAPLGQFP 20

RESULT 14
US-10-296-734-978
; Sequence 978, Application US/10296734
; Publication No. US2004005417A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2015
; CURRENT APPLICATION NUMBER: US/10/253,286
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; NUMBER OF SEQ ID NOS: 905

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; TITLE OF INVENTION: Synthetic molecules and uses therefor

; FILE REFERENCE: Savine

; CURRENT APPLICATION NUMBER: US/10/296,734

; CURRENT FILING DATE: 2003-08-04

; PRIORITY NUMBER: AU PQ7761/00

; PRIOR FILING DATE: 2000-05-26

; NUMBER OF SEQ ID NOS: 1507

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO: 978

; LENGTH: 30

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: tyros segment 4  
US-10-296-734-978

Query Match 100.0%; Score 79; DB 12; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Name/Key: QY 1 QNILLSNAPLGQQFP 15

Db 13 QNILLSNAPLGQQFP 27

RESULT 15

US-10-253-286-525

; Sequence 525, Application US/10253286

; Publication No. US20040058881A1

; GENERAL INFORMATION:

; APPLICANT: HUMPHREYS, ROBERT

; TITLE OF INVENTION: Li-key/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES

; FILE REFERENCE: REH 2015

; CURRENT APPLICATION NUMBER: US/10/253,286

; CURRENT FILING DATE: 2003-01-13

; PRIORITY NUMBER: 10/197,000

; PRIOR FILING DATE: 2002-07-17

; PRIOR APPLICATION NUMBER: 09/396,813

; PRIOR FILING DATE: 1999-09-14

; NUMBER OF SEQ ID NOS: 905

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO: 525

; LENGTH: 32

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Li-key/tyrosinase non-overlapping hybrid peptide

; FEATURE:

; NAME/KEY: MOD\_RES

; LOCATION: (5)

; OTHER INFORMATION: a-aminovaleric acid

; FEATURE:

; OTHER INFORMATION: C-term amidated

US-10-253-286-525

Query Match 100.0%; Score 79; DB 12; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Name/Key: QY 1 QNILLSNAPLGQQFP 15

Db 18 QNILLSNAPLGQQFP 32

Search completed: June 3, 2004, 15:24:22  
Job time : 39 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2004, 17:05:32 ; Search time 29 Seconds  
(without alignments)  
26.703 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_56\_70  
Perfect score: 79  
Sequence: 1 QNLLISNAPLGQPFP 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Parents AA:  
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2: /cgns2\_6/\_ptodata/2/iaa/5B\_COMB.pep:  
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4: /cgns2\_6/\_ptodata/2/iaa/6B\_COMB.pep:  
5: /cgns2\_6/\_ptodata/2/iaa/PCHTUS\_COMB.pep:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution and is derived by analysis of the result being printed.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	15	2 US-09-036-582-22	Sequence 22, Appl
2	79	100.0	15	3 US-09-183-706-25	Sequence 25, Appl
3	79	100.0	15	4 US-09-166-448-66	Sequence 66, Appl
4	79	100.0	15	4 US-09-567-995-25	Sequence 25, Appl
5	79	100.0	15	4 US-09-165-863-22	Sequence 22, Appl
6	79	100.0	15	4 US-09-009-953-198	Sequence 198, Appl
7	79	100.0	15	4 US-09-697-884-66	Sequence 66, Appl
8	79	100.0	15	4 US-09-289-350-22	Sequence 22, Appl
9	79	100.0	15	4 US-09-574-749B-24	Sequence 24, Appl
10	79	100.0	15	4 US-09-318-141-22	Sequence 22, Appl
11	79	100.0	15	4 US-09-601-729-112	Sequence 112, Appl
12	79	100.0	15	4 US-07-891-942G-10	Sequence 10, Appl
13	79	100.0	15	4 US-07-891-942G-8	Sequence 8, Appl
14	79	100.0	15	2 US-08-370-909-19	Sequence 19, Appl
15	79	100.0	15	4 US-08-504-048-8	Sequence 8, Appl
16	79	100.0	15	4 US-09-341-982-1	Sequence 1, Appl
17	79	100.0	15	4 US-09-169-717E-39	Sequence 39, Appl
18	79	100.0	15	4 US-10-011-36-4	Sequence 4, Appl
19	79	100.0	15	3 US-08-540-922D-12	Sequence 12, Appl
20	79	100.0	15	1 US-07-891-942G-5	Sequence 5, Appl
21	72	91.1	15	4 US-09-169-717E-28	Sequence 28, Appl
22	66	83.5	13	2 US-08-902-516-41	Sequence 41, Appl
23	66	83.5	13	4 US-09-847-185-41	Sequence 41, Appl
24	45	57.0	263	4 US-09-134-001C-4512	Sequence 4512, Appl
25	42	53.2	923	4 US-09-252-991A-271A8	Sequence 271A8, Appl
26	40	50.6	124	4 US-09-134-000C-4402	Sequence 4402, Appl
27	40	50.6	170	4 US-09-107-532A-7110	Sequence 7110, Appl

## ALIGNMENTS

RESULT 1 **OK**  
US-09-036-582-22  
; Sequence 22, Application US/09036582A  
; Patent No. 5965381  
; GENERAL INFORMATION:  
; APPLICANT: van der Bruggen, Pierre  
; TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS  
; TITLE OF INVENTION: WITH RECOMBINANT YERSINIA  
; FILE REFERENCE: 111.54  
; CURRENT APPLICATION NUMBER: US-09-036-582A  
; CURRENT FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 22  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Human Tyrosinase peptide

RESULT 2  
US-09-183-706-25  
; Sequence 25, Application US/09183706  
; Patent No. 6245525  
; GENERAL INFORMATION:  
; APPLICANT: Martelange, Valrie  
; APPLICANT: De Smet, Charles  
; APPLICANT: Boon-Pailleur, Thierry  
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
; FILE REFERENCE: L0461/7054  
; CURRENT APPLICATION NUMBER: US/09/183, 706  
; CURRENT FILING DATE: 1998-03-30  
; EARLIER APPLICATION NUMBER: 09/1122, 989  
; EARLIER FILING DATE: 1999-07-27  
; NUMBER OF SEQ ID NOS: 43  
; SEQ ID NO: 25  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-183-706-25  
; Sequence 25, Application US/09183706  
; Patent No. 6245525  
; GENERAL INFORMATION:  
; APPLICANT: Martelange, Valrie  
; APPLICANT: De Smet, Charles  
; APPLICANT: Boon-Pailleur, Thierry  
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
; FILE REFERENCE: L0461/7054  
; CURRENT APPLICATION NUMBER: US/09/183, 706  
; CURRENT FILING DATE: 1998-03-30  
; EARLIER APPLICATION NUMBER: 09/1122, 989  
; EARLIER FILING DATE: 1999-07-27  
; NUMBER OF SEQ ID NOS: 43  
; SEQ ID NO: 25  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-183-706-25  
; Sequence 25, Application US/09183706  
; Patent No. 6245525  
; GENERAL INFORMATION:  
; APPLICANT: Martelange, Valrie  
; APPLICANT: De Smet, Charles  
; APPLICANT: Boon-Pailleur, Thierry  
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
; FILE REFERENCE: L0461/7054  
; CURRENT APPLICATION NUMBER: US/09/183, 706  
; CURRENT FILING DATE: 1998-03-30  
; EARLIER APPLICATION NUMBER: 09/1122, 989  
; EARLIER FILING DATE: 1999-07-27  
; NUMBER OF SEQ ID NOS: 43  
; SEQ ID NO: 25  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens

Query Match 100.0%; Score 79; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQFP 15  
 Db 1 QNILLSNAPLGQFP 15

RESULT 3 OK

Sequence 66 Application US/09166448  
 Patent No. 6291430  
 GENERAL INFORMATION:  
 APPLICANT: Chaux, Pascal  
 APPLICANT: Vantomme, Vairie  
 APPLICANT: Stroobant, Vincent  
 APPLICANT: Boon-Falleur, Thierry  
 APPLICANT: van der Bruggen, Pierre  
 APPLICANT: Thielemans, Kris  
 APPLICANT: Corthals, Jurgen  
 TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
 CURRENT APPLICATION NUMBER: US/09/166,448  
 CURRENT FILING DATE: 1998-10-05  
 NUMBER OF SEQ ID NOS: 81  
 SOFTWARE: Fastseq for Windows Version 3.0  
 SEQ ID NO 66 LENGTH: 15 TYPE: PRT  
 ORGANISM: Homo sapiens US-09-166-448-66

Query Match 100.0%; Score 79; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQFP 15  
 Db 1 QNILLSNAPLGQFP 15

OK Gln Asn Ile Leu Ser Asp Ala Pro Leu Gly Pro Gln Phe Pro

RESULT 4 OK

Sequence 25 Application US/09567995  
 Patent No. 6303756  
 GENERAL INFORMATION:  
 APPLICANT: Martelange, Val, rie  
 APPLICANT: De Smet, Charles  
 APPLICANT: Boon-Falleur, Thierry  
 TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
 CURRENT APPLICATION NUMBER: US/09/567,995  
 CURRENT FILING DATE: 2000-05-10  
 PRIOR APPLICATION NUMBER: 09/183,706  
 PRIOR FILING DATE: 1998-10-30  
 NUMBER OF SEQ ID NOS: 43  
 SEQ ID NO 25 LENGTH: 15 TYPE: PRT  
 ORGANISM: Homo sapiens US-09-567-995-25

Query Match 100.0%; Score 79; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQFP 15  
 Db 1 QNILLSNAPLGQFP 15

RESULT 5

OK

US-09-165-863-22 Sequence 22 Application US/09165863  
 Patent No. 6407063  
 GENERAL INFORMATION:  
 APPLICANT: Luitjen, Rosalie  
 APPLICANT: Duffour, Marie-Therese  
 APPLICANT: Demotte, Nathalie  
 APPLICANT: van der Bruggen, Pierre  
 APPLICANT: Cornelis, Guy  
 APPLICANT: Stroobant, Vincent  
 APPLICANT: Lurquin, Christophe  
 APPLICANT: Boon-Falleur, Thierry  
 APPLICANT: Chaux, Pascal  
 TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL PROCEDURE  
 FILE REFERENCE: 11727  
 CURRENT APPLICATION NUMBER: US/09/165,863  
 CURRENT FILING DATE: 1999-10-02  
 NUMBER OF SEQ ID NOS: 45  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 22 LENGTH: 15 TYPE: PRT  
 ORGANISM: Human Tyrosinase peptide US-09-165-863-22

Query Match 100.0%; Score 79; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQFP 15  
 Db 1 QNILLSNAPLGQFP 15

OK

RESULT 6 OK

US-09-009-053-198 Sequence 198 Application US/09009953  
 Patent No. 6413517  
 GENERAL INFORMATION:  
 APPLICANT: Sette, Alessandro  
 TITLE OF INVENTION: Identification of Broadly Reactive DR Restricted Epitopes  
 NUMBER OF SEQUENCES: 274  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ FOR WINDOWS VERSION 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/009,953  
 FILING DATE: 21-Jan-1998  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/036,713  
 FILING DATE: 23-JAN-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Weber, Ellen Lauver  
 REGISTRATION NUMBER: 32,762  
 REFERENCE/DOCKET NUMBER: 018623-011520US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-576-0200  
 TELEFAX: 415-576-0300  
 TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 198:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 198:  
 US-09-009-53-198

Query Match 100.0%; Score 79; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QNILLSNAPLGQFQP 15  
 Db 1 QNILLSNAPLGQFQP 15

RESULT 7  
 US-09-697-884-66

OK

Sequence 66, Application US/09697884  
 Patent No. 6426217  
 GENERAL INFORMATION:  
 APPLICANT: Chaux, Pascal  
 Vantomme, Valérie  
 Stroobant, Vincent  
 Boon-Falleur, Thierry  
 van der Bruggen, Pierre  
 Thielemans, Kris  
 CORTHALS, Jurgen  
 TITLE OF INVENTION: MAGB-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
 FILE REFERENCE: L0461/7052  
 CURRENT APPLICATION NUMBER: US/09/697,884  
 CURRENT FILING DATE: 2000-10-27  
 PRIOR APPLICATION NUMBER: 09/165,448  
 PRIOR FILING DATE: 1998-10-05  
 NUMBER OF SEQ ID NOS: 81  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 66  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-697-884-66

Query Match 100.0%; Score 79; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QNILLSNAPLGQFQP 15  
 Db 1 QNILLSNAPLGQFQP 15

RESULT 8  
 US-09-289-350-22

OK

Sequence 22, Application US/09289350  
 Patent No. 6511451  
 GENERAL INFORMATION:  
 APPLICANT: Chaux, Pascal  
 Luiken, Rosalie  
 Demotte, Nathalie  
 Deffour, Marie-Therese  
 Lurquin, Christophe  
 Traversari, Catia  
 Stroobant, Vincent  
 Cornelis, Guy R.  
 Boon-Falleur, Thierry  
 Van Der Bruggen, Pierre  
 CORNEILIS, Guy R.  
 TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL PROCEDURE  
 FILE REFERENCE: 117272  
 CURRENT APPLICATION NUMBER: US/09/289,350

INFORMATION FOR SEQ ID NO: 198:  
 CURRENT FILING DATE: 1999-04-09  
 PRIORITY CLAIMS:  
 PRIORITY FILING DATE: 1998-10-02  
 NUMBER OF SEQ ID NOS: 49  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 22  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Human Tyrosinase peptide  
 US-09-289-350-22

RESULT 9  
 US-09-574-749B-24

OK

Sequence 24, Application US/09574749B  
 Patent No. 6548299  
 GENERAL INFORMATION:  
 APPLICANT: ROSENWEIG, Michael  
 PYKETT, Mark J.  
 SCADDEN, David T.  
 POZNANSKY, Mark C.  
 TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION  
 FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL  
 TITLE OF INVENTION: DEVICES  
 FILE REFERENCE: C1005/7012/XA/ERG  
 CURRENT APPLICATION NUMBER: US/09/574,749B  
 CURRENT FILING DATE: 2002-05-21  
 PRIOR APPLICATION NUMBER: US 60/107,972  
 PRIOR FILING DATE: 1998-11-12  
 PRIOR APPLICATION NUMBER: PCT/US99/26795  
 PRIOR FILING DATE: 1999-11-12  
 PRIOR APPLICATION NUMBER: US 09/524,749  
 NUMBER OF SEQ ID NOS: 58  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 24  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Homo Sapiens Source  
 US-09-574-749B-24

Query Match 100.0%; Score 79; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNILLSNAPLGQFQP 15  
 Db 1 QNILLSNAPLGQFQP 15

RESULT 10  
 US-09-318-141-22

OK

Sequence 22, Application US/09318141  
 Patent No. 6602505  
 GENERAL INFORMATION:  
 APPLICANT: van der Bruggen, Pierre  
 CORNELIS, Guy R.  
 TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS  
 WITH RECOMBINANT YERSINIA  
 FILE REFERENCE: 111154  
 CURRENT APPLICATION NUMBER: US/09/318,141  
 CURRENT FILING DATE: 1999-05-25  
 EARLIER APPLICATION NUMBER: US 09/036,582

; EARLIER FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 22  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Human Tyrosinase peptide  
; US-09-318-141-22

Query Match 100.0%; Score 79; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 QNILLSNAPLGQFP 15  
 Db 1 QNILLSNAPLGQFP 15

RESULT 11  
 US-09-601-729-112  
 Sequence 112, Application US/09601729  
 Patent No. 6683052  
 GENERAL INFORMATION:  
 APPLICANT: THIAM, KADER  
 APPLICANT: AURIACUT, CLAUDE  
 APPLICANT: GRAS-MASSE, HELENE  
 APPLICANT: LOING, ESTELLE  
 APPLICANT: VERWAERDE, CLAUDIE  
 APPLICANT: GUILLET, JEAN GERARD

TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES  
 FILE REFERENCE: USB-97-AU-IN  
 CURRENT APPLICATION NUMBER: US/09/601,729  
 CURRENT FILING DATE: 2000-11-20  
 PRIOR APPLICATION NUMBER: PCT/FR99/00259  
 PRIOR FILING DATE: 1999-02-05  
 PRIOR APPLICATION NUMBER: 98 01439  
 PRIOR FILING DATE: 1998-02-06  
 NUMBER OF SEQ ID NOS: 281  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 112  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-601-729-112  
 Query Match 100.0%; Score 79; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 QNILLSNAPLGQFP 15  
 Db 1 QNILLSNAPLGQFP 15

Query Match 100.0%; Score 79; DB 1; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQFP 15  
 Db 56 QNILLSNAPLGQFP 70

RESULT 13  
 US-07-891-942G-8  
 Sequence 8, Application US/07891942G  
 Patent No. 5679511  
 GENERAL INFORMATION:  
 APPLICANT: KWON, Byoung Se  
 TITLE OF INVENTION: cDNA CLONES FOR HUMAN TYROSINASE AND FOR  
 TITLE OF INVENTION: A REGULATORY PROTEIN IN THE MELANIN PROTEIN PATHWAY  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Christopher A. Michaelis, Barnard, Brown &

STREET: 306 East State Street, Suite 220  
 CITY: Ithaca  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 14850  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/891,942G  
 FILING DATE: 01-JUN-1992  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 06/915,753  
 FILING DATE: 06-OCT-1986  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/362,847  
 FILING DATE: 07-JUN-1989

RESULT 12  
 US-07-891-942G-10  
 Sequence 10, Application US/07891942G  
 Patent No. 5679511  
 GENERAL INFORMATION:  
 APPLICANT: KWON, Byoung Se  
 TITLE OF INVENTION: cDNA CLONES FOR HUMAN TYROSINASE AND FOR  
 TITLE OF INVENTION: A REGULATORY PROTEIN IN THE MELANIN PROTEIN PATHWAY  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Christopher A. Michaelis, Barnard, Brown &  
 STREET: 306 East State Street, Suite 220  
 CITY: Ithaca  
 STATE: NY

ATTORNEY/AGENT INFORMATION:  
 NAME: Michaels, Christopher A  
 REGISTRATION NUMBER: 34,390  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 607-273-2659  
 TELEFAX: 607-273-1711  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 529 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-07-891-942G-8

Query Match 100.0%; Score 79; DB 1; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQFP 15  
 Db 56 QNILLSNAPLGQFP 70

RESULT 14  
 US-08-370-909-19  
 Sequence 19, Application US/08370909  
 GENERAL INFORMATION:  
 Patent No. 5843648  
 APPLICANT: ROBBINS, PAUL F.; ROSENBERG,  
 APPLICANT: STEVEN A.  
 TITLE OF INVENTION: P15 AND TYROSINASE  
 TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC  
 TITLE OF INVENTION: AND THERAPEUTIC METHODS  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
 STREET: 345 PARK AVENUE  
 CITY: NEW YORK  
 STATE: NEW YORK  
 COUNTRY: USA  
 ZIP: 10154

COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/370,909  
 FILING DATE: 10-JAN-1995  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: CAROL M. GRUPPI  
 REGISTRATION NUMBER: 37,341  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 758-4800  
 TELEX: 421792  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 529  
 STRANDEDNESS: UNKNOWN  
 TOPOLOGY: UNKNOWN  
 MOLECULE TYPE: PROTEIN  
 US-08-370-909-19

Query Match 100.0%; Score 79; DB 2; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQFP 15

Db 56 QNILLSNAPLGQFP 70

RESULT 15  
 US-08-504-048-8  
 Sequence 8, Application US/08504048  
 ; Patent No. 583674  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TAKIMOTO, Hironuki  
 ; APPLICANT: SUZUKI, Satoshi  
 ; APPLICANT: SHIBATA, Koushi  
 ; APPLICANT: MASUI, Shigeaki  
 ; TITLE OF INVENTION: ANTI-HUMAN TYROSINASE  
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODY  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Knobbe, Martens, Olson & Bear  
 ; STREET: 620 Newport Center Drive 16th Floor  
 ; CITY: Newport Beach  
 ; STATE: CA  
 ; COUNTRY: U.S.A.  
 ; ZIP: 92660  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSEQ Version 1.5  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/504,048  
 ; FILING DATE:  
 ; CLASSIFICATION: 436  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Altman, Daniel E.  
 ; REGISTRATION NUMBER: 34,115  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 714-760-0404  
 ; TELEFAX: 714-760-9502  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 529 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOBETICAL: NO  
 ; ANTI-SENSE: NO  
 ; FRAGMENT TYPE: internal  
 ; ORIGINAL SOURCE:  
 ; US-08-504-048-8

Query Match 100.0%; Score 79; DB 2; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQFP 15  
 Db 56 QNILLSNAPLGQFP 70

RESULT 16  
 US-09-341-982-1  
 Sequence 1, Application US/09341982  
 ; Patent No. 6588671  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SLINGUFF, Craig L.  
 ; APPLICANT: HUNT, Donald F.  
 ; APPLICANT: ENGELHARD, Victor H.

APPLICANT: KITTELESEN, David  
 TITLE OF INVENTION: CYTOKINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED  
 FILE REFERENCE: SLINGLUFF=3B  
 CURRENT APPLICATION NUMBER: US/09/341,982  
 EARLIER APPLICATION NUMBER: PCT/US98/01592  
 EARLIER FILING DATE: 1998-01-29  
 EARLIER APPLICATION NUMBER: 60/037,781  
 EARLIER FILING DATE: 1997-01-31  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 1  
 LENGTH: 529  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-341-982-1

RESULT 17  
 Query Match Score 79; DB 4; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	QNILLSNAPLGQQFP 15	
Db	56	QNILLSNAPLGQQFP 70	

APPLICANT: Ooms, Annie  
 APPLICANT: DeGiovanni, Gerard  
 APPLICANT: Morel, Sandra  
 APPLICANT: Van den Eynde, Benoit  
 APPLICANT: Boon-Falleur, Thierry  
 TITLE OF INVENTION: Isolate Peptides Which Bind To HLA-B35 Molecules,  
 TITLE OF INVENTION: Larger Peptides Which Contain These, Nucleic Acid  
 FILE REFERENCE: JUDG=561  
 CURRENT APPLICATION NUMBER: US/09/169,717E  
 CURRENT FILING DATE: 1998-10-09  
 NUMBER OF SEQ ID NOS: 39  
 SEQ ID NO 39  
 LENGTH: 529  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 US-09-169-717E-39

Query Match Score 79; DB 4; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	QNILLSNAPLGQQFP 15	
Db	56	QNILLSNAPLGQQFP 70	

RESULT 18  
 Query Match Score 79; DB 4; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	QNILLSNAPLGQQFP 15	
Db	56	QNILLSNAPLGQQFP 70	

GENERAL INFORMATION:  
 US-10-011-436-4  
 Sequence 4, Application US/1001436  
 Patent No. 666946  
 APPLICANT: Boon-Falleur, Thierry; Brichard, Vincent; Van Pel,  
 Aline; DePlaen, Etienne; Coulie, Pierre; Renaud, Jean Christophe; Wolfe,  
 Lethie, Bernard  
 TITLE OF INVENTION: METHOD FOR IDENTIFYING INDIVIDUALS SUFFERING FROM  
 A CELLULAR ABNORMALITY SOME OF WHOSE ABNORMAL CELLS PRESENT  
 LEUKOCYTE

NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fullbright & Jaworski L.L.P.  
 STREET: 801 Pennsylvania Avenue N.W.  
 CITY: Washington  
 STATE: District of Columbia  
 COUNTRY: USA  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.25inch, 1.44MB storage  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: PC-DOS  
 SOFTWARE: Wordperfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/011,436  
 FILING DATE: 11-Dec-2001  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/511,011  
 FILING DATE: 5-AUGUST-1995  
 APPLICATION NUMBER: 08/054,714  
 FILING DATE: 28-APRIL-1993  
 APPLICATION NUMBER: 07/994,928  
 FILING DATE: 22-DECEMBER-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mary Anne Schofield  
 REGISTRATION NUMBER: 36,669  
 REFERENCE/DOCKET NUMBER: LUD 5299.9 DIV CON  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 662-0200  
 TELEFAX: (202) 662-4643  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 529  
 TYPE: amino acids  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
 US-10-011-436-4  
 Query Match Score 100.0%; Score 79; DB 4; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-05; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 QNILLSNAPLGQQFP 15  
 Dd 56 QNILLSNAPLGQQFP 70  
 RESULT 19  
 US-08-540-922D-12  
 Sequence 12, Application US/08540922D  
 Patent No. 6284476  
 GENERAL INFORMATION:  
 APPLICANT: Boon-Falleur, Thierry; Brichard, Vincent; Van Pel,  
 Aline; DePlaen, Etienne; Coulie, Pierre;  
 APPLICANT: Renaud, Jean-Christophe; Wolfe, Thomas; and  
 APPLICANT: Lethie, Bernard  
 TITLE OF INVENTION: METHOD OF IDENTIFYING INDIVIDUALS SUFFERING  
 FROM A CELLULAR ABNORMALITY SOME OF WHOSE  
 ABNORMAL CELLS PRESENT COMPLEXES OF HUMAN  
 LEUKOCYTE ANTIGEN TYROSINASE DERIVED  
 PEPTIDES, AND METHODS FOR TREATING SAID  
 INDIVIDUALS  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSSEE: Felfe & Lynch  
 STREET: 805 Third Avenue  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10022  
 COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: PC-DOS  
 SOFTWARE: Wordperfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/540,922D  
 FILING DATE: October 11, 1995  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/054,714  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/994,928  
 FILING DATE: December 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mary Anne Schofield  
 REGISTRATION NUMBER: 36,669  
 REFERENCE DOCKET NUMBER: LUD 5299.5  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 688-9200  
 TELEFAX: (212) 838-3884  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 537  
 STRANDEDNESS: single  
 STRAND: +  
 TOPOLogy: linear  
 US-08-540-922D-12

Query Match Score 79; DB 3; Length 537;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-05;  
 Matches 15; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy	1 QNILLSNAPLGQFP 15
Db	64 QNILLSNAPLGQFP 78

## RESULT 20

US-07-891-942G-5  
 Sequence 5, Application US/07891942G  
 Patent No. 5679511  
 GENERAL INFORMATION:  
 APPLICANT: Kwon, Byoung Se  
 TITLE OF INVENTION: cDNA CLONES FOR HUMAN TYROSINASE AND FOR  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Christopher A. Michaels, Barnard, Brown &  
 STREET: 306 East State Street; Suite 220  
 CITY: Ithaca  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 14850  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/891,942G  
 FILING DATE: 01-JUN-1992  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 06/915,753  
 FILING DATE: 06-OCT-1986  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/362,847  
 FILING DATE: 07-JUN-1989  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Michael, Christopher A  
 REGISTRATION NUMBER: 34,390



Copyright (c) 1993 - 2004 Compugen Ltd.	GenCore version 5.1.6	30	21	23.3	11	2	D37196
OM protein - protein search, using sw model		31	21	23.3	11	2	PN0042
Run on:	June 3, 2004, 15:23:00 ; Search time 21 Seconds (without alignments)	32	21	23.3	12	2	PH1462
Title:	US-08-533-895A-39_COPY_56_72	33	21	23.3	13	2	D61491
Perfect score:	90	34	21	23.3	15	2	S27248
Sequence:	1 QNLISNAPIGLQPQFPT 17	35	20.5	22.8	15	2	JN0730
Scoring table:	BLOSUM62	36	20	22.2	8	2	E47393
Gapopen:	10.0 , Gapext 0.5	37	20	22.2	8	2	A28719
Searched:	283366 seqs, 96191526 residues	38	20	22.2	9	2	R28495
Total number of hits satisfying chosen parameters:	2772	39	20	22.2	10	1	XASNPC
Minimum DB seq length: 0		40	20	22.2	13	2	A28953
Maximum DB seq length: 16		41	20	22.2	13	2	S13273
Post-processing: Minimum Match 0% Maximum Match 100%		42	20	22.2	14	2	361309
Database :	PIR_78;* 1: pir1;* 2: pir2;* 3: pir3;* 4: pir4;*	43	20	22.2	14	2	C48394
Scored:	283366 seqs, 96191526 residues	44	20	22.2	15	2	A285115
Result No.	Score	Query Match	Length	DB ID	Description	Indels	O; Gaps
1	27	30.0	9	2 A61364	isotocin - common Ig heavy chain DJ	0;	O;
2	27	30.0	16	2 PH1302	oxytocin - hippopo oxytocin - spotted oxytocin - finback oxytocin - Australian oxytocin - rabbit	3	ISNCPTG 9
3	25	27.8	9	2 A91466	chaperone, TCP1-re granulocyte-e-colony		
4	25	27.8	9	2 A92774	diuretic neuropept		
5	25	27.8	9	2 B93147	cycloleuconinin -		
6	25	27.8	9	2 A93408	bradykinin-potenti		
7	25	27.8	9	2 B90667	natin - rape (frag		
8	25	27.8	14	2 S3802	2S albumin large C		
9	24	26.7	8	4 I54017	collagen alpha 1 cha		
10	24	26.7	9	2 A29477	dystrophin-associa		
11	23.5	26.1	12	2 JU336	hypothetical 1.5K		
12	23	25.6	11	1 XAVIBH	cytochrome P450 1F		
13	23	25.6	12	2 S67328	agiotensin-conver		
14	23	25.6	13	2 S09716	85K glycoprotein -		
15	23	25.6	14	2 S23376	serine protease		
16	23	25.6	14	2 PN0666	milk band B protei		
17	23	25.6	15	2 B39109	locustapokinin -		
18	23	25.6	16	2 E41425	T-cell receptor -		
19	22	24.4	13	1 XAVIB	dystrophin-associa		
20	22	24.4	13	2 S3273	T-cell receptor be		
21	22	24.4	15	2 PN0144	translation elonga		
22	22	24.4	15	2 C61511	alpha-2-macroglobu		
23	22	24.4	16	1 A49761	bradykinin-potenti		
24	22	24.4	16	2 D49125			
25	21.5	23.9	12	2 PN0663			
26	21	23.3	8	2 PT0530			
27	21	23.3	9	2 D58503			
28	21	23.3	9	2 S66635			
29	21	23.3	11	2 C37196			

A91466  
 oxytocin - hippocotamus neurophysin I  
 N;Contains: neurophysin 1; oxytocin  
 C;Species: Hippopotamus amphibius (hippopotamus)  
 C;Date: 30-Oct-1992 #sequence revision 30-Oct-1992 #text\_change 20-Mar-1998  
 C;Accession: A91466; A01450; B01450  
 R;Ferguson, D.R.; Pickering, B.T.  
 Gen. Comp. Endocrinol. 13, 425-429, 1969  
 A;Title: Arginine and lysine vasoressins in the hippopotamus neurohypophysis.  
 A;Reference number: A91466; MUID:71232719; PMID:5406077  
 A;Accession: A91466  
 A;Molecule type: protein  
 A;Residues: 1-9 <PBR>  
 C;Comment: Oxytocin is followed by neurophysin 1 in the precursor.  
 C;Superfamily: oxytocin-neurophysin  
 C;Keywords: amidated carboxyl end; hormone; hypothalamus  
 F;1-6/Disulfide bonds: #status predicted  
 F;9/Modified site: amidated carboxyl end (Gly) #status predicted

Query Match Score 27.8%; Score 25; DB 2; Length 9;  
 Best Local Similarity 57.1%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 LSNAPLG 11  
 Db : |||  
 3 IQNCPLG 9

RESULT 6  
 A91408  
 oxytocin - Australian echidna  
 N;Alternate names: neurophysin I  
 C;Species: Tachyglossus aculeatus (Australian echidna)  
 C;Accession: A93408; A01450; B01450  
 R;Acher, R.; Chauvet, J.; Chauvet, M.T.  
 Nature New Biol. 244, 124-126, 1973  
 A;Title: Neurohypophysial hormones and evolution of tetrapods.  
 A;Reference number: A91408; MUID:73223515; PMID:4515919  
 A;Accession: A93408  
 A;Molecule type: protein  
 A;Residues: 1-9 <ACH>  
 C;Comment: Oxytocin is followed by neurophysin 1 in the precursor.  
 C;Superfamily: oxytocin-neurophysin  
 C;Keywords: amidated carboxyl end; hormone; hypothalamus  
 F;1-6/Disulfide bonds: #status predicted  
 F;9/Modified site: amidated carboxyl end (Gly) #status predicted

Query Match Score 27.8%; Score 25; DB 2; Length 9;  
 Best Local Similarity 57.1%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 LSNAPLG 11  
 Db : |||  
 3 IQNCPLG 9

RESULT 7  
 B90667  
 oxytocin - rabbit  
 N;Alternate names: neurophysin I  
 N;Contains: neurophysin 1; oxytocin  
 C;Species: Oryctolagus cuniculus (domestic rabbit)  
 C;Accession: B90667; A01450; B01450  
 R;Chauvet, J.; Chauvet, M.T.; Acher, R.  
 Biochimie 53, 1099-1104, 1971  
 A;Title: Evolution des hormones neurohypophysaires: isolement des principes actifs du lait  
 A;Accession number: A90667; MUID:72215050; PMID:5150741  
 A;Molecule type: protein  
 A;Residues: 1-9 <CHA>  
 C;Comment: Oxytocin is followed by neurophysin 1 in the precursor.  
 C;Superfamily: oxytocin-neurophysin  
 C;Keywords: amidated carboxyl end; hormone; hypothalamus  
 F;1-6/Disulfide bonds: #status experimental  
 F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match Score 27.8%; Score 25; DB 2; Length 9;  
 Best Local Similarity 57.1%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 LSNAPLG 11  
 Db : |||

A;Residues: 1-9 <ACH>  
 C;Comment: Oxytocin is followed by neurophysin 1 in the precursor.  
 C;Superfamily: oxytocin-neurophysin  
 C;Keywords: amidated carboxyl end; hormone; hypothalamus  
 F;1-6/Disulfide bonds: #status experimental  
 F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match Score 27.8%; Score 25; DB 2; Length 9;  
 Best Local Similarity 57.1%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 LSNAPLG 11  
 Db : |||  
 3 IQNCPLG 9

RESULT 6  
 A91408  
 oxytocin - Australian echidna  
 N;Alternate names: neurophysin I  
 C;Species: Tachyglossus aculeatus (Australian echidna)  
 C;Accession: A93408; A01450; B01450  
 R;Acher, R.; Chauvet, J.; Chauvet, M.T.  
 Nature New Biol. 244, 124-126, 1973  
 A;Title: Neurohypophysial hormones and evolution of tetrapods.  
 A;Reference number: A91408; MUID:73223515; PMID:4515919  
 A;Accession: A93408  
 A;Molecule type: protein  
 A;Residues: 1-9 <ACH>  
 C;Comment: Oxytocin is followed by neurophysin 1 in the precursor.  
 C;Superfamily: oxytocin-neurophysin  
 C;Keywords: amidated carboxyl end; hormone; hypothalamus  
 F;1-6/Disulfide bonds: #status predicted  
 F;9/Modified site: amidated carboxyl end (Gly) #status predicted

Query Match Score 27.8%; Score 25; DB 2; Length 9;  
 Best Local Similarity 57.1%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 LSNAPLG 11  
 Db : |||  
 3 IQNCPLG 9

RESULT 7  
 B90667  
 oxytocin - rabbit  
 N;Alternate names: neurophysin I  
 N;Contains: neurophysin 1; oxytocin  
 C;Species: Oryctolagus cuniculus (domestic rabbit)  
 C;Accession: B90667; A01450; B01450  
 R;Chauvet, J.; Chauvet, M.T.; Acher, R.  
 Biochimie 53, 1099-1104, 1971  
 A;Title: Evolution des hormones neurohypophysaires: isolement des principes actifs du lait  
 A;Accession number: A90667; MUID:72215050; PMID:5150741  
 A;Molecule type: protein  
 A;Residues: 1-9 <CHA>  
 C;Comment: Oxytocin is followed by neurophysin 1 in the precursor.  
 C;Superfamily: oxytocin-neurophysin  
 C;Keywords: amidated carboxyl end; hormone; hypothalamus  
 F;1-6/Disulfide bonds: #status experimental  
 F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match Score 27.8%; Score 25; DB 2; Length 9;  
 Best Local Similarity 57.1%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 LSNAPLG 11  
 Db : |||

Db	3 IONCPLG 9	Qy	4 LLISNAPIG 11
S33802	RESULT 8	Db	2 LITNCPRG 9
chaperone, TOP1-related - oat			
C;Species: Avena sativa (oat)			
C;Date: 02-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 17-Mar-1999			
C;Accession: S33802			
R;Mummert, E.; Grimm, R.; Speth, V.; Eckerskorn, C.; Schiltz, E.; Gatenby, A.A.; Schaeffer, Nature 363, 644-648, 1993	RESULT 11	JU0356	cycloleouminin - sagebrush motherwort
A;Title: A TOP1-related molecular chaperone from plants refolds phytochrome to its photo		C;Species: Leonurus japonicus (sagebrush motherwort)	
A;Reference number: S33800; MUID:93288140; PMID:8093715		C;Accession: JU0356	#text_change 16-Jul-1999
A;Accession: S33802		R;Kinoshita, K.; Tanaka, J.; Kuroda, K.; Natori, S.; Kinoshita, T.	
A;Status: preliminary		A;Title: Cycloleouminin, a cyclic Peptide from Leonuri fructus.	
A;Molecule type: protein		A;Reference number: JU0356; MUID:31300597; PMID:2070452	
A;Residues: 1-14 <MOM>		A;Accession: JU0356	
Query Match 27.8%; Score 25; DB 2; Length 14;		A;Status: preliminary	
Best Local Similarity 62.5%; Pred. No. 4e+02;		A;Molecule type: protein	
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;		A;Residues: 1-12 <KIN>	
Qy 5 LSNAIPLGP 12	Qy	9 PLGP-QFP 15	
Db 2 LSAKLGP 9	Db	3 PAGPTQYP 10	
RESULT 9			
granulocyte-colony stimulating factor precursor - synthetic (fragment)			
C;Species: synthetic			
A;Note: human gene engineered and expressed in Escherichia coli			
C;Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 28-Jan-2000		XAVITH	bradykinin-potentiating peptide - halys viper
C;Accession: 154017		N;Alternate names: BPP	
R;Devlin, P.E.; Drummond, R.J.; Toy, P.; Marx, D.F.; Watt, K.W.; Devlin, J.J.		C;Species: Agkistrodon halys (halys viper)	
Gene 65, 13-22, 1988		C;Accession: 30-Sep-1988 #sequence_revision 30-Sep-1988	#text_change 05-Aug-1994
A;Title: Alteration of amino-terminal codons of human granulocyte-colony-stimulating fac		R;Chi, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.	
i.		Peptides 6, 333-342, 1985	
A;Reference number: 154017; MUID:88284374; PMID:2456256		A;Title: Structure-function studies on the bradykinin potentiating peptide from Chinese	
A;Accession: 154017		A;Reference number: JC0002; MUID:86177022; PMID:3008123	
A;Status: translated from GB/EMBL/DBJ		A;Accession: JC0002	
A;Molecule type: mRNA		A;Molecule type: protein	
A;Residues: 1-8 <DEV>		A;Residues: 1-11 <CRH>	
A;Cross-references: GB:MB20922; NID:98066318; PIDN:AAA66353.1; PID:9183043		C;Comment: Because this peptide both inhibits the activity of the angiotensin-converting	
Query Match 26.7%; Score 24; DB 4; Length 8;		C;Superfamily: bradykinin-potentiating peptide	
Best Local Similarity 100.0%; Pred. No. 2.8e+05;		C;Keywords: angiotensin-converting enzyme inhibitor; antihypertensives; bradykinin; pyrog	
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		F;1;Modified site: pyrrolidine carboxylic acid (Gln) #status experimental	
Qy 9 PLGP 12	Qy	9 PLGPQFP 15	
Db 3 PLGP 6	Db	4 PPGPPTP 10	
RESULT 10			
diuretic neuropeptide F1 - migratory locust			
C;Species: Locusta migratoria (migratory locust)		RESULT 13	
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1993		S67528	narin - rape (fragments)
C;Accession: A29477		C;Species: Brassica napus (rape)	
R;Proux, J.P.; Miller, C.A.; Li, J.P.; Carney, R.L.; Girardie, A.; Delaage, M.; Schooley, Biochem. Biophys. Res. Commun. 149, 180-186, 1987		C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997	#text_change 13-Mar-1997
A;Title: Identification of arginine vasopressin-like diuretic hormone from Locusta mi		R;Muren, B.; Ek, B.; Rask, L.	
A;Reference number: A29477; PMID:8807077; PMID:3689410		Bur. J. Biochem. 227, 316-321, 1995	
A;Accession: A29477		A;Title: Processing of the 2S storage protein pronarin in Brassica napus and in transfor	
A;Molecule type: protein		A;Reference number: S67528; MUID:95154306; PMID:7851402	
A;Residues: 1-9 <PRO>		A;Accession: S67528	
A;Note: two neuropeptides, F1 and F2, were identified. F2 is an antiparallel dimer of F1		A;Status: preliminary	
C;Keywords: neuropeptide		A;Molecule type: protein	
Query Match 26.7%; Score 24; DB 2; Length 9;		A;Residues: 1-6;7-12 <MUR>	
Best Local Similarity 50.0%; Pred. No. 2.8e+05;			
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;			

Query Match 25.6%; Score 23; DB 2; Length 12;  
 Best Local Similarity 80.0%; Pred. No. 7.4e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 9 PLGPQ 13  
 Db 7 PQGPQ 11

## RESULT 14

S09716  
 2S albumin large chain (1 and 2) nII - rape (fragments)  
 N;Alternate names: 2S albumin large chain nIII  
 C;Species: Brassica napus (rape)  
 C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text\_change 21-Aug-1998  
 C;Accession: S09716; S09718; S09717  
 R;Monsalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.  
 FEBS Lett. 267, 209-212, 1990  
 A;Title: beta-Turns as structural motifs for the proteolytic processing of seed proteins  
 A;Reference number: S09720; MUID:90242974; PMID:2185951  
 A;Accession: S09716  
 A;Molecule type: protein  
 A;Residues: 1-9;10-13 <M01>  
 A;Experimental source: seed  
 A;Note: 3-Ser was also found  
 A;Accession: S09718  
 A;Molecule type: protein  
 A;Residues: 1-9;10-13 <M02>  
 A;Experimental source: seed  
 A;Accession: S09717  
 A;Molecule type: protein  
 A;Residues: 1-9;10-13 <M03>  
 A;Experimental source: seed

Query Match 25.6%; Score 23; DB 2; Length 13;  
 Best Local Similarity 80.0%; Pred. No. 8.2e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 9 PLGPQ 13  
 Db 7 PQGPQ 5

## RESULT 15

S23376  
 collagen alpha chain - polychaete (*Alvinella pompejana*) (fragment)  
 C;Species: Alvinella pompejana  
 C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 29-May-1998  
 C;Accession: S23376  
 R;Guill, F.; Wiedemann, H.; Mann, K.; Kuehn, K.; Timpl, R.; Engel, J.  
*J. Mol. Biol.* 221, 209-223, 1991  
 A;Title: Molecular characterization of cuticle and interstitial collagens from worms co-  
 A;Reference number: S17381; MUID:920405; PMID:1920405  
 A;Accession: S23376  
 A;Molecule type: protein  
 A;Residues: 1-14 <GAI>

Query Match 25.6%; Score 23; DB 2; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 8.9e+02;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 PLGPQ 13  
 Db 7 PMGPR 11

Search completed: June 3, 2004, 15:27:17  
 Job time : 22 secs

Result No.	Score	Query	Match	Length	DB	ID	Description
1	28	31.1	16	1	H5_COTAJA	P18338	coturnix co
2	27	30.0	9	1	ISOT_CYPCA	P42939	cyprinus ca
3	26	28.9	9	1	OXYA_SQUAC	P42999	squalus acca
4	25	27.8	9	1	OXYT_RABIT	P32878	oryctolagus cuniculus
5	24	26.7	9	1	DNEF_LOCMI	P16339	locusta migratoria
6	23	25.6	9	1	OXYA_SCYCA	P42996	scylliorhinus scylliorhinus
7	23	25.6	9	1	OXYT_RAJCL	P42994	raja clavata
8	23	25.6	11	1	BPP_AKGHP	P04562	agkistrodon piscivorus
9	23	25.6	15	1	CYSK_CLOPA	P13340	clostridium botulinum
10	22	24.4	9	1	OXYV_SQUAC	P43000	squalus acanthias
11	22	24.4	9	1	UPA3_HUMAN	P30089	homo sapiens
12	22	24.4	13	1	BPP1_BOTJA	P01200	bothrops jararaca
13	22	24.4	15	1	SODM_ENTA	P22799	entecobacillus entecobacter
14	22	24.4	16	1	LPKL_LOCMI	P20404	locusta migratoria
15	21	23.3	9	1	OXYF_SCYCA	P42997	scylliorhinus scylliorhinus
16	21	23.3	9	1	OXYT_OCTVU	P80027	octopus vulgaris
17	21	23.3	11	1	BPP3_BOTIN	P30423	bothrops inornatus
18	21	23.3	11	1	BPP4_BOTIN	P30424	bothrops inornatus
19	21	23.3	13	1	LMAL1_LOCMI	P38496	locusta migratoria
20	20	22.2	8	1	AL5_CALVO	P41841	calliphora vomitoria
21	20	22.2	8	1	PAR7_ASCSU	P43171	ascaris suum
22	20	22.2	9	1	CONO_CONST	P05487	conus striatus
23	20	22.2	10	1	BPP_VIPAS	P31351	vipera aspis
24	20	22.2	14	1	TAT_HV1W2	P1209	human immunodeficiency virus type 1
25	20	22.2	14	1	TAT_HV1Z8	P12511	human immunodeficiency virus type 2
26	20	22.2	15	1	GLN2_PINPS	P81107	pinus pinaster
27	19	21.1	9	1	OXYT_CYPCA	P22879	cyprinus carpio
28	19	21.1	9	1	UPA7_HUMAN	P30093	homo sapiens
29	19	21.1	10	1	BPP2_BOTIN	P30422	bothrops inornatus
30	19	21.1	10	1	BPP2_BOTJA	P01022	bothrops jararaca
31	19	21.1	13	1	BOM1_PSEGU	P42991	bombyx mori
32	19	21.1	14	1	CALL_CALGI	P20728	calotropis gigantea
33	19	21.1	14	1	UN46_CLOPA	P81362	clostridium perfringens

Scoring table:	BLOSUM62
Gapop:	10.0
Gapext:	0.5
Searched:	141681 seqs., 52070155 residues
Total number of hits satisfying chosen parameters:	880
Minimum DB seq length:	0
Maximum DB seq length:	16
Post-processing: Minimum Match 0%	Maximum Match 100%
Database :	SwissProt_42.*
Scoring table:	Gapop 10.0 , Gapext 0.5

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query	Match	Length	DB	ID
1	28	31.1	16	1	H5_COTAJA	P18338
2	27	30.0	9	1	ISOT_CYPCA	P42939
3	26	28.9	9	1	OXYA_SQUAC	P42999
4	25	27.8	9	1	OXYT_RABIT	P32878
5	24	26.7	9	1	DNEF_LOCMI	P16339
6	23	25.6	9	1	OXYA_SCYCA	P42996
7	23	25.6	9	1	OXYT_RAJCL	P42994
8	23	25.6	11	1	BPP_AKGHP	P04562
9	23	25.6	15	1	CYSK_CLOPA	P13340
10	22	24.4	9	1	OXYV_SQUAC	P43000
11	22	24.4	9	1	UPA3_HUMAN	P30089
12	22	24.4	13	1	BPP1_BOTJA	P01200
13	22	24.4	15	1	SODM_ENTA	P22799
14	22	24.4	16	1	LPKL_LOCMI	P20404
15	21	23.3	9	1	OXYF_SCYCA	P42997
16	21	23.3	9	1	OXYT_OCTVU	P80027
17	21	23.3	11	1	BPP3_BOTIN	P30423
18	21	23.3	11	1	BPP4_BOTIN	P30424
19	21	23.3	13	1	LMAL1_LOCMI	P38496
20	20	22.2	8	1	AL5_CALVO	P41841
21	20	22.2	8	1	PAR7_ASCSU	P43171
22	20	22.2	9	1	CONO_CONST	P05487
23	20	22.2	10	1	BPP_VIPAS	P31351
24	20	22.2	14	1	TAT_HV1W2	P1209
25	20	22.2	14	1	TAT_HV1Z8	P12511
26	20	22.2	15	1	GLN2_PINPS	P81107
27	19	21.1	9	1	OXYT_CYPCA	P22879
28	19	21.1	9	1	UPA7_HUMAN	P30093
29	19	21.1	10	1	BPP2_BOTIN	P30422
30	19	21.1	10	1	BPP2_BOTJA	P01022
31	19	21.1	13	1	BOM1_PSEGU	P42991
32	19	21.1	14	1	CALL_CALGI	P20728
33	19	21.1	14	1	UN46_CLOPA	P81362

ALIGNMENTS							
<b>RESULT 1</b>							
H5_COTAJA	H5_COTAJA	STANDARD;	PRT;	16 AA.			
ID	H5_COTAJA	AC	P18338;				
		DT	01-NOV-1990 (Rel. 16, Created)				
		DT	01-NOV-1990 (Rel. 16, Last sequence update)				
		DT	15-JUL-1999 (Rel. 38, Last annotation update)				
		DE	Histone H5 (Fragment).				
		OS	Coturnix coturnix japonica (Japanese quail).				
		OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Coturnix.				
		NCBI_TaxID	93934; [1]				
		RN					
		SEQUENCE.					
		RX	SEQUENCE.				
		RA	RELINE V., Roy C.; Dove M.; Yaguchi M.;				
		RT	"Species variability of N-terminal sequence of avian erythrocyte-specific histone H5."				
		RL	Biochem Biophys Res Commun. 71:196-202(1976).				
		CC	-!- FUNCTION: HISTONE H5 PERFORMS THE SAME FUNCTION AS H1, BEING NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES, AND REPLACES HISTONE H1 IN CERTAIN CELLS.				
		CC	-!- SUBCELLULAR LOCATION: Nuclear.				
		CC	-!- TISSUE SPECIFICITY: Thyroid cells.				
		CC	-!- SIMILARITY: Belongs to the histone H1/H5 family.				
		KW	CHROMOSOMAL PROTEIN; Nuclear protein; DNA-binding; DNA condensation.				
		FT	NON TER	16			
		SO	SEQUENCE	16 AA;	1665 MW;	DB52821B3074D3C CRC64;	
						Score 28;	DB 1;
						Length 16;	
						Best Local Similarity	31.1%;
						Mismatches	3.85%;
						5;	Indels
						0;	Gaps
		QY	1 QNTILSNPLGPQ 13				
		DB	::::          : 2 ESIVLSPAPK 14				
<b>RESULT 2</b>							
ISOT_CYPCA	ISOT_CYPCA	STANDARD;	PRT;	9 AA.			
ID	P2293;	AC					
		DT	01-NOV-1995 (Rel. 32, Created)				
		DT	01-NOV-1995 (Rel. 32, Last sequence update)				
		DT	01-NOV-1995 (Rel. 32, Last annotation update)				
		DE	Isotocin.				
		OS	Cyprinus carpio (Common carp).				
		OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Cypriniformes;				
		OC	Cyprinidae; Cyprinus.				
		NCBI_TaxID	1962; [1]				
		RN					
		RP	SEQUENCE.				
		RC	TISSUE.				
		RA	ACHER R., CHAUVEAU J., CHAUVEAU M.-T., CREPY D.;				

RT "Characterization of neurohypophyseal hormones from a freshwater bony fish, the carp (*Cyprinus carpio*). Comparison with hormones from sea water bony fishes." ;

RT water bony fishs." ;

RL Comp. Biochem. Physiol. 14: 245-254 (1965). .

CC !- SIMILARITY: ANTIURETIC HORMONE.

-!- SIMILARITY: Belongs to the vasopressin/oxytocin family.

DR PIR: A61364; A61364.

DR InterPro: IPR00981; Neurhyp\_norm.

DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.

KW Hormone; Amidation.

FT DISULFID 1 6 AMIDATION.

FT MOD RES 9 9 AMIDATION.

SQ SEQUENCE 9 AA; 969 MW; 17FF476EB455B04B CRC64;

Query Match Score 30.0%; Score 27; DB 1; Length 9;

Best Local Similarity 57.1%; Pred. No. 1.4e+05; Indels 0; Gaps 0;

Matches 4; Conservative 2; Mismatches 1; Indels 0;

QY 5 LSNAPLG 11

Db 3 INNCPLG 9

RP SEQUENCE 3

OXYA\_SQUAC STANDARD; PRT; 9 AA.

ID OXYA\_SQUAC AC P42999;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DB Aspartocin (Asparagocin).

OS Squalus acanthias (Spiny dogfish).

OC Blasmodibranchii; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

OC Squalidae; Squalae; Squaloidei; Squalidae; Squalus.

NCBI\_TAXID=7797;

RN RX MEDLINE=73031727; PubMed=5083097;

RA Achér R., Chauvet M.-T., Chaubet J., Fontaine M.;

RT "Phylogeny of the neurohypophyseal hormones. Two new active peptides isolated from a cartilaginous fish, *Squalus acanthias*." ;

RL Bur. J. Biochem. 29:12-19(1972).

RN [2]

RP SEQUENCE. MEDLINE=722128038; PubMed=622083;

RA Achér R., Chauvet J., Chauvet M.-T., Fontaine M.;

RT "Identification of 2 new neurohypophyseal hormones, valitocin (Val8-oxytocin) and asparocin (Asn8-oxytocin) in a selachian fish, the spiny dogfish (*Squalus acanthias*)";

RL C. R. Acad. Sci. ,D. Sci. Nat. 274:313-316(1972).

CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.

DR InterPro: IPR00981; Neurhyp\_norm.

DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.

KW Hormone; Amidation.

FT DISULFID 1 6 AMIDATION.

FT MOD RES 9 9 AMIDATION.

SQ SEQUENCE 9 AA; 969 MW; 17FB376B44404B CRC64;

Query Match Score 28.9%; Score 26; DB 1; Length 9;

Best Local Similarity 57.1%; Pred. No. 1.4e+05; Indels 0; Gaps 0;

Matches 4; Conservative 2; Mismatches 1;

QY 5 LSNAPLG 11

Db 3 INNCPLG 9

RESULT 4

OXYT\_RABIT STANDARD; PRT; 9 AA.

AC P32878; P01188;

AC P32878; P01188;

AC P32878; P01188;

AC P32878; P01188;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DB Oxytocin (Ocytocin).

CC Orcytocinus cuniculus (Rabbit).

CS Hippopotamus amphibius (Hippopotamus).

CS Balaenoptera physalus (Finback whale) ('Common rorqual'),

CS Hydrocytus aculeatus aculeatus (Austral echidna), and

CS Tachyglossus aculeatus aculeatus (Spotted ratfish) ('Pacific ratfish').

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Leporiformes.

CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae.

CO NCBI\_TAXID=9986; 9833; 9770; 49271; 7873;

CX [1] \_MOD\_TAXID=9986;

RN RN SEQUENCE.

RC RC SPECIES=H\_amphibius;

RC RC SPECIES=H\_amphibius;

RC RC SPECIES=H\_amphibius;

RC RC SPECIES=B\_physalis;

RC RC SPECIES=B\_physalis;

RC RC SPECIES=A\_aculeatus;

Db	3 IONCPLG	9	
<b>RESULT 5</b>			
DNF1 LOCMI ID _DNF1 LOCMI	STANDARD;	PRT;	9 AA.
AC P16339;			
DT 01-AUG-1990 (Rel. 15, Created)			
DT 01-AUG-1990 (Rel. 15, Last sequence update)			
DT 10-OCT-2003 (Rel. 42, Last annotation update)			
DB Locupressin (Diuretic neuropeptide F1/F2).			
OS Locusta migratoria (Migratory locust).			
OC Neoptera; Orthopteroidea; Orthoptera; Hexapoda; Insecta; Pterygota;			
OC Acridoidea; Acrididae; Oedipodinae; Locusta.			
OX NCBI_TAXID=7004;			
RN [1]			
RP SEQUENCE.			
RC TISSUE_Suboesophageal ganglion, and thoracic ganglion;			
RX MEDLINE=88070707; PubMed=3689410;			
RA Proux J.-P., Miller C.A., Li J.P., Carney R.L., Girardie A.,			
RA Delaage M., Schooley D.A.;			
RT "Identification of an arginine vasopressin-like diuretic hormone from Locusta migratoria."			
RT Biochem. Biophys. Res. Commun. 149:180-186 (1987).			
RL Biochem. Biophys. Res. Commun. 149:180-186 (1987).			
CC - - FUNCTION: DIURETIC HORMONE.			
CC - - SUBUNIT: Monomer (F1) and homodimer (F2); disulfide-linked.			
CC - - SIMILARITY: Belongs to the vasopressin/oxytocin family.			
CC - - SIMILARITY: Belongs to the vasopressin/oxytocin family.			
DR PIR: A29477; A29477.			
DR InterPro: IPR000981; Neurhyp_horm.			
DR PFAM: PF00220; hormone; 1.			
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.			
KW Hormone; Neuropeptide; Amidation.			
FT DISULFID 1 6 IN F1.			
FT DISULFID 1 1 INTERCHAIN (WITH C-6) (IN F2).			
FT DISULFID 6 6 INTERCHAIN (WITH C-1) (IN F2).			
FT MOD_RES 9 9 AMIDATION.			
SQ SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;			
Query Match Score 24; DB 1; Length 9;			
Best Local Similarity 50.0%; Pred. No. 1.4e+05;			
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;			
DR			
Qy 4 LSNSAPLG 11			
Db 2 LITNCPRG 9			
<b>RESULT 6</b>			
OXYA_SCYCA ID_OXYA_SCYCA	STANDARD;	PRT;	9 AA.
AC P42956;			
DT 01-NOV-1995 (Rel. 32, Created)			
DT 01-NOV-1995 (Rel. 32, Last sequence update)			
DE Asvacocin.			
OS Scylliorhinus canicula (Spotted dogfish) (Spotted catshark)			
OC Eulambrachii; Chordata; Craniata; Vertebrata; Chondrichthyes;			
OC Scylliorhinidae; Scylliorhinus.			
OX NCBI_TAXID=7830;			
RN [1]			
RP SEQUENCE.			
RC TISSUE=Pituitary;			
RX MEDLINE=95062247; PubMed=7972045;			
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.,			
RT "Special evolution of neurohypophysis hormones in cartilaginous fishes: avatocin and phasmatocin, two oxytocin-like peptides isolated from the spotted dogfish (Scylliorhinus caniculus).";			
RT Proc. Natl. Acad. Sci. U.S.A. 91:1266-1270 (1994).			
CC - - FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.			
CC - - SIMILARITY: Belongs to the vasopressin/oxytocin family.			
DR InterPro: IPR000981; Neurhyp_horm.			
DR			
Qy 5 LSNSAPLG 11			
Db 3 ISNCFQG 9			
<b>RESULT 8</b>			
BPP_AGPKHP ID_BPP_AGPKHP	STANDARD;	PRT;	11 AA.
AC P04562;			
DT 13-ANG-1987 (Rel. 05, Created)			
DT 01-FEB-1994 (Rel. 28, Last sequence update)			
DT 28-FEB-2003 (Rel. 41, Last annotation update)			
DB Bradykinin-Potentiating Peptide (Angiotensin-converting enzyme inhibitor).			
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys pallas).			
OC Eulambrachii; Chordata; Craniata; Vertebrata; Butelostomii; Lepidosauria; Squamata; Scincoglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Gloydius.			
OC NCBI_TAXID=8714;			
RN [1]			
RP SEQUENCE.			

RESULT 9  
 TISSUE=Venom;  
 RX MEDLINE=9617022; PubMed=3008123;  
 RA Chi C.-W.; Wang S.-Z.; Xu L.-G.; Wang M.-Y.; Lo S.-S.; Huang W.-D.;  
 RT "Structure-function studies on the bradykinin potentiating peptide from Chinese snake venom (Agkistrodon halys pallas).";  
 RT Peptides 6 Suppl. 3:339-342(1985).  
 -|- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR: JCC002; XAVIBH.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 11 AA; 1112 MW;

Query Match Score 23; DB 1; Length 11;  
 Best Local Similarity 57.1%; Pred. No. 4.4e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PLGFQFP 15  
 DB 4 PPGPIP 10

RESULT 9  
 CYSK\_CLOPA  
 ID CYSK\_CLOPA STANDARD; PRT; 15 AA.  
 AC P81340;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Cysteine synthase (EC 2.5.1.47) (O-acetylserine sulfhydrylase) (O-acetylserine (thiol)-lyase) (CSSae) (CP 27) (Fragment).  
 DE CN CYSK.  
 OS Clostridium pasteurianum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OC NCBI\_TaxID=1501;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=W5;  
 RX MEDLINE=98291870; PubMed=9629918;  
 RA Plengsrud R.; Skjeldal L.;  
 RT "Two-dimensional gel electrophoresis separation and N-terminal sequence analysis of proteins from Clostridium pasteurianum W5.";  
 RL Electrophoresis 19:812-806(1998).  
 -|- CATALYTIC ACTIVITY: O(3)-acetyl-L-serine + H(2)S = L-Cysteine + acetate.  
 CC |- COFACTOR: Pyridoxal phosphate (By similarity).  
 CC |- PATHWAY: Cysteine biosynthesis.  
 CC |- SUBUNIT: Homodimer (By similarity).  
 CC |- SIMILARITY: Belongs to the cysteine synthase/cystathione beta-synthase family.  
 CC DR InterPro: IPR001216; Cys synthase\_BS.  
 DR PROSITE; PS00901; CYSINE\_SYNTHASE; PARTIAL.  
 KW Transerase; Cysteine\_biosynthesis; Pyridoxal phosphate.  
 FT NON TER 15 15  
 SQ SEQUENCE 15 AA; 1625 MW; 01965828967A352 CRC44;

Query Match Score 23; DB 1; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 6.3e+02;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 LISNAPL 10  
 DB 5 IIGNTP1 11

RESULT 10  
 OXYV\_SQUAC  
 ID OXYV\_SQUAC STANDARD; PRT; 9 AA.  
 AC P43000;  
 DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DE 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Valitocin  
 OS Squalus acanthias (Spiny dogfish).  
 OC Blasmatrachia; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Blasmobranchii; Squalidae; Squaloidei; Squalus; Squalus.  
 NCBI\_TaxID=7797;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=73031727; PubMed=5083083;  
 RA Achter R.; Chauvet J.; Chauvet M.-T.; Fontaine M.;  
 RT "Identification of 2 new neurohypophyseal hormones, valitocin (Val8-oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the spiny dog-fish (Squalus acanthias).";  
 RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).  
 CC |- SIMILARITY: Belongs to the vasopressin/oxytocin family.  
 DR InterPro: IPR000981; Neurhyp\_horm.  
 DR Pfam; PF00220; hormone4\_1.  
 DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
 RW Hormone: Amidation.  
 PT DISULFID 1 6  
 PT MOD RES 9 9  
 SQ SEQUENCE 9 AA; 996 MW; 17E0D7EB45SD04B CRC64;  
 Query Match Score 22; DB 1; Length 9;  
 Best Local Similarity 42.9%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Qy 5 LISNAPL 11  
 DB 3 IQNCPVG 9

RESULT 11  
 UPA3\_HUMAN STANDARD; PRT;  
 ID UPA3\_HUMAN STANDARD; PRT;  
 AC P30059;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown Protein from 2D-page of plasma (Spot 11) (Fragment).  
 DE Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buthidae; Primates; Catarrhini; Homiridae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=93092937; PubMed=1459097;  
 RA Sanchez J.-C.; James R.; Paquet N.; Ravier F.; Pasquali C.; Hochstrasser D.P.; Hughes G.J.; Frutiger S.; Paquet N.; Bjellqvist B.,  
 RT "Plasma protein map: an update by microsequencing.";  
 RL Electrophoresis 13:707-714(1992).  
 CC |- MISCELLANEOUS: On the 2D-gel the determined PI of this unknown protein is: 4.6, its MW is: 46 kDa.  
 CC SWISS-2DPAGE; P30059; HUMAN.  
 DR NON\_TER 1 1  
 PT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;  
 Query Match Score 22; DB 1; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 12 PQPFPT 17

Db 2 PLFPXT 7

RESULT 12

ID BPPI\_BOTIA STANDARD; PRT; 13 AA.

AC P01020; B30421; PRT; 13 AA.

CC -I- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.

CC -I- CATALYTIC ACTIVITY: 2 superoxide + 2 H<sub>+</sub> = O<sub>2</sub> + H<sub>2</sub>O (2).

CC -I- COFACTOR: Blinds 1 iron ion per subunit (BY similarity).

CC -I- SUBUNIT: Homodimer.

CC -I- SIMILARITY: Belongs to the iron/manganese superoxide dismutase family.

DR PIR; PN0615; PN0615.

DR InterPro; IPR00189; SODISmutase.

DR Pfam; PP00081; sod1; 1.

DR PROSITE; PS00088; SOD MN; PARTIAL.

KW Oxidoreductase; Metal-binding; Iron.

PT NON\_TER 15 15

SQ SEQUENCE 15 AA; 1756 MW; 352F3D949202B642 CRC64;

Query Match 24.4%; Score 22; DB 1; Length 15;

Best Local Similarity 60.0%; Pred. No. 9.3e+02;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 PQPFF 16

Db 5 PQDPY 9

RESULT 14

ID LPK1\_LOCMI STANDARD; PRT; 16 AA.

AC P20404;

DR 01-FEB-1991 (Rel. 17, Created)

DR 01-FEB-1994 (Rel. 28, Last sequence update)

DR 28-FEB-2003 (Rel. 41, Last annotation update)

DB Locustapyrokinin 1 (LOM-PK-1).

OS Locusta migratoria (Migratory locust).

OS Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acrideromorpha;

OC Acrideridae; Acriidae; Oedipodinae; Locusta.

NCBI\_TaxID=7004; [1]

DR RN

RP SEQUENCE.

RX SPECIES=B. jararaca; TISSUE=Venom;

RX MEDLINE=72118526; PubMed=4334402;

RX Ondetti M.A., Williams N.J., Sabo E.F., Plussec J., Weaver B.R.,

RX Kocy O.;

RX "Angiotensin-converting enzyme inhibitors from the venom of Bothrops jararaca. Isolation, elucidation of structure, and synthesis.";

RX Biochemistry 10:4033-4039 (1971).

RN [2]

RP SEQUENCE.

RC SPECIES=B. insularis; TISSUE=Venom;

RX MEDLINE=90351557; PubMed=238615;

RX Cintra A.C., Vieira C.A., Giglio J.R.;

RT "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";

RT J. Protein Chem. 9: 221-227 (1990).

CC -I- FUNCTION: This Peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that deactivate it.

CC IT acts as an indirect hypotensive agent.

DR PIR; A01253; XAV19B.

RX Hypotensive agent; Pyrrolidone carboxylic acid.

FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

SQ SEQUENCE 13 AA; 1388 MW;

Query Match 24.4%; Score 22; DB 1; Length 13;

Best Local Similarity 60.0%; Pred. No. 7.9e+02;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GPOPF 15

Db 8 GPEEP 12

RESULT 13

ID SODM\_ENTAE STANDARD; PRT; 15 AA.

AC P22759;

DR 01-AUG-1991 (Rel. 19, Created)

DR 01-AUG-1991 (Rel. 19, Last sequence update)

DR 10-OCT-2003 (Rel. 42, Last annotation update)

GN SODA.

OS Enterobacter aerogenes (Aerobacter aerogenes). Bacteroidales; Enterobacteriaceae; Enterobacter.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacter.

OC NCBI\_TaxID=548;

RN [1]

RP SEQUENCE.

RX MEDLINE=91248479; PubMed=1368558;

RX Kim S.W., Lee S.O., Lee T.H.;

RT Purification and characterization of superoxide dismutase from Aerobacter aerogenes.";

RT Aerobacter aerogenes.

RESULT 15

ID OXYF\_SCYCA STANDARD; PRT; 9 AA.

AC P42957;

DR OXYF\_SCYCA

DR InterPro; IPR001484; Pyrokinin.

DR PROSITE; PS00539; PYROKININ; 1.

RX Schools L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;

RX "Isolation, primary structure, and synthesis of locustapyrokinin: a myotropic peptide of Locusta migratoria."

RX Gen. Comp. Endocrinol. 81:97-104 (1991).

CC -I- FUNCTION: Mediates visceral muscle contractile activity (myotropic activity).

CC -I- SIMILARITY: Belongs to the pyrokinin family.

DR PIR; A49761; A49761.

DR InterPro; IPR001484; Pyrokinin.

DR PROSITE; PS00539; PYROKININ; 1.

RX Neuropeptide; Amidation; Pyrokinin, Pyrrolidone carboxylic acid.

FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD\_RES 16 16 AMIDATION.

SQ SEQUENCE 16 AA; 1827 MW; A7178BBDC0AFDD6 CRC64;

Query Match 24.4%; Score 22; DB 1; Length 16;

Best Local Similarity 80.0%; Pred. No. 1e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 PQPFF 16

Db 8 PQDPY 12

DE Phasvatocin.  
 OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark)  
 OC Bukaryota; Metazoa; Chordata; Craniata; vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;  
 OC Scyliorhinidae; Scyliorhinus.  
 OX NCBI\_TaxID=7830;  
 RN [1]  
 RP  
 SEQUENCE  
 TISSUE=Pituitary;  
 RC MEDLINE=55062247; PubMed=7972045;  
 RX  
 RA Chauvet J., Bouille Y., Chauveau C., Chauvet M.-T., Achier R.;  
 RT "Special evolution of neurohypophyseal hormones in cartilaginous  
 fishes: avsotocin and phasvatocin, two oxytocin-like peptides  
 isolated from the spotted dogfish (Scyliorhinus caniculus).";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270 (1994).  
 CC -!- FUNCTION: DISPLAYS OXYTOCIN ACTIVITY ON RAT UTERUS.  
 DR InterPro:IPR000981; Neurhyp-horm.  
 DR Pfam: PF00220; hormone; 1.  
 PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone /  
 FT Hormone / Amidation.  
 FT DISULFID 1 6  
 FT MOD RES 9 9 AMIDATION  
 SQ SEQUENCE 9 AA; 1016 MW; 17EDD76EB4449DB CRC64;  
 QY Query Match 23.3%; Score 21; DB 1; Length 9;  
 Best Local Similarity 50.0%; Pred: No. 1.4e+05;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Db 6 SNAPLG 11  
 Db 4 NNCPVG 9

Search completed: June 3, 2004, 15:25:51  
 Job time : 11 secs

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OM protein - protein search, using sw model

Run on: June 3, 2004, 15:22:20 ; Search time 39 Seconds

(without alignments)  
137.534 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_56\_72

Perfect score: 1 QNTLNSNPLGPQPFT 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_25:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_minc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rabbit:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_virus:\*

16: sp\_bacteriap:\*

17: sp\_archeap:\*

17 21 23.3 12 2 Q8KZ86 acinetobact

Q85G95 pyrrhobryum 18 21 23.3 12 8 Q85G95

PB1801 streptomyce 19 21 23.3 14 2 PB1801

Q85G97 pyrrhobryum 20 21 23.3 14 8 Q85G97

Q85G92 pyrrhobryum 21 21 23.3 14 8 Q85G92

Q51436 pseudomonas 22 21 23.3 16 2 Q51436

Q80B26 hepatitis b 23 20.5 22.8 11 12 Q80B26

Q8mjg0 saginatus fu 24 20.5 22.8 12 6 Q8mjg0

Q8mjpb calimico g 25 20.5 22.8 12 6 Q8mjpb

Q8mjpt callithrix 26 20.5 22.8 12 6 Q8mjpt

Q8mjpv leontopithecus 27 20.5 22.8 12 6 Q8mjpv

Q8mjq3 saimiri sci 28 20.5 22.8 12 6 Q8mjq3

Q8mjq1 atelles fusc 29 20.5 22.8 12 6 Q8mjq1

Q8mjje2 cebus apella 30 20.5 22.8 12 6 Q8mjje2

Q87624 roux sarcom 31 20 22.2 7 15 Q87624

Q90y93 gallus gallus 32 20 22.2 10 13 Q90y93

P90442 spodoptera 33 20 22.2 13 12 P90442

Q95i17 escherichia 34 20 22.2 14 2 Q95i17

O70539 rattus norvegicus 35 20 22.2 14 11 O70539

Q8jdm3 human immunodeficiency virus 36 20 22.2 14 15 Q8jdm3

Q8jdmt7 human immunodeficiency virus 37 20 22.2 14 15 Q8jdmt7

Q8jdmo human immunodeficiency virus 38 20 22.2 14 15 Q8jdmo

Q69353 herpes simplex 39 20 22.2 15 12 Q69353

Q54894 mus musculus 40 20 22.2 16 11 Q54894

Q9jams rattus norvegicus 41 20 22.2 16 11 Q9jams

Q9rjy3 mus musculus 42 20 22.2 16 11 Q9rjy3

Q9tr99 canis familiaris 43 19.5 21.7 16 6 Q9tr99

Q8hu42 passiflora 44 19.5 21.7 16 8 Q8hu42

Q8hu29 passiflora 45 19.5 21.7 16 8 Q8hu29

### ALIGNMENTS

**RESULT 1**  
Q8NHY1 PRELIMINARY; PRT; 16 AA.  
ID Q8NHY1; AC Q8NHY1;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DB Hepatic nuclear factor regulatory circuit in differentiated  
pancreatic cells;  
GN HNFPA.  
OS Homo sapiens (Human).  
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RN [1] NCBI\_TAXID=9606;  
RN [1] SEQUENCE FROM N.A.  
RN Boj S.F., Parrizas M., Ferrer J.i.  
RN MEDLINE=21592951; PubMed=11717395;  
RN Boj S.F., Parrizas M., Maestro M.A., Ferrer J.i.  
RN "A transcription factor regulatory circuit in differentiated  
pancreatic cells";  
RN Proc. Natl. Acad. Sci. U.S.A. 98:14481-14486 (2001).  
RN [2] SEQUENCE FROM N.A.  
RN Boj S.F., Parrizas M., Ferrer J.i.  
RN RHEV4A expression in human pancreatic cells";  
RN Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP509467; AAC34296.2; -.  
FT NON\_TER 16  
SQ SEQUENCE 16 AA; 1621 MW; 1F4CE5EB61FF009 CRC64;

Query Match Score 27; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

%

Query Match Length DB ID Description

Result No.	Score	Match	Length	DB	ID	Description
1	27	30.0	16	4	Q8NHY1	Q8dhy1 homo sapien
2	26	28.9	15	6	Q9TRN8	Q9trn8 sus scrofa
3	25	27.8	11	2	Q48933	Q48933 mycobacteri
4	25	27.8	12	6	P83127	P83127 bos indicus
5	25	27.8	16	6	077489	077489 tupaias glis
6	24	26.7	11	2	087882	087882 mycobacteri
7	24	26.7	13	10	Q43174	Q43174 solanum tub
8	24	26.7	15	6	Q9TR03	Q9tr03 bos taurus
9	23	25.6	16	5	Q9TWK1	Q9twk1 mytilus edulis
10	23	25.6	16	5	Q9TWK0	Q9twk0 mytilus edulis
11	22	24.4	10	10	P82438	P82438 nicotiana tabacum
12	22	24.4	14	2	P81715	P81715 streptomyce
13	22	24.4	15	6	Q9TRN7	Q9trn7 sus scrofa
14	22	24.4	16	10	Q8RVF4	Q8rvf4 zea mays (m)
15	21	23.3	7	3	P83492	P83492 bionectria
16	21	23.3	11	12	Q8QGP0	Q8qgp0 tomato leaf

RESULT 2

7 NAPIG 11  
5 NAPIG 9  
Db  
OY



Matches	5;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;	Qy	9 PLGQFPF 16	Db	3 PGSQDPF 10
<b>RESULT 6</b>													
ID	O87882	PRELIMINARY;	PRT;	11 AA.						Qy	7 NAPLGQPF 14	Db	3 NDPNNGPMY 10
AC	O87882;												
DT	01-NOV-1998	(TREMBLrel. 08, Created)											
DT	01-NOV-1998	(TREMBLrel. 08, Last sequence update)											
DT	01-NOV-1998	(TREMBLrel. 08, Last annotation update)											
DE	AlkyI hydroperoxide reductase (Fragment).												
GN	AHPC.												
OS	Mycobacterium xenopii.												
OC	Bacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Mycobacterium.												
OX	NCBI_TaxID=1789;												
RN	[1]												
SEQUENCE FROM N.A.													
RC	STRAIN=ATCC19250;												
RX	MEDLINE=98446038; PubMed=9733688;												
RA	Pagan-Ramos E., Song J., McFalone M., Mudd M.H., Deretic V.; "Oxidative stress response and characterization of the oxyR-ahpC and furA-katG loci in Mycobacterium marinum.";												
RT	J. Bacteriol. 180:4855-4864(1998).												
RL	EMBL; U43810; AAC61663..1; -.												
DR	NON-TER 11 AA;												
SQ	SEQUENCE 11 AA; 1147 MW;												
Query Match													
Best Local Similarity	26.7%	Score 24;	DB 2;	Length 11;						Qy	9 PLGQFP 15		
Matches	4;	Conservative	1;	Mismatches 1;	Indels	0;	Gaps	0;		Db	5 PNGPNLP 11		
Best Local Similarity													
Matches	4;	Conservative	1;	Mismatches 1;	Indels	0;	Gaps	0;					
Qy	10 LGQFP 15												
Db	6 IGGQFP 11												
<b>RESULT 7</b>													
Q43174	PRELIMINARY;												
ID	Q43174;	PRT;	13 AA.										
AC	01-NOV-1996 (TREMBLrel. 01, Created)												
DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)												
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)												
DE	Beta-fructofuranosidase (EC 3.2.1.26) (Fragment).												
OS	Solanum tuberosum (potato).												
OC	Spermatophytina; Streptophytina; Embryophytina; Tracheophytina; Lamiales; Solanales; Solanaceae; Solanum.												
OC	Core eudicots; asterids;												
OC	Core eudicots; asterids;												
RN	[1]												
SEQUENCE FROM N.A.													
RC	MEDLINE=96779736; PubMed=8710506;												
RA	Bourney A.S., Hedley P.E., Maddison A., Waugh R., Machray G.C.; "Exon skipping induced by cold stress in a potato invertase gene transcript."												
RT	Nucleic Acids Res. 24:2347-2351 (1996).												
RL	EMBL; X95B11; CRA65081..1; -.												
DR	GO:0004564; F:beta-fructofuranosidase activity; IEA.												
DR	GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.												
DR	GO:00055375; P:carbohydrate metabolism; IEA.												
KW	Glycosidase; Hydrolase.												
FT	NON-TER 1	1	13	13									
FT	NON-TER 13	13 AA;	1541 MW;	1B3053E7384C6874 CRC64;									
SQ	SEQUENCE 13 AA;												
<b>RESULT 8</b>													
Q9TR03	PRELIMINARY;												
ID	Q9TR03;	PRT;	15 AA.										
AC	01-MAY-2000 (TREMBLrel. 13, Created)												
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)												
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)												
DE	Neuron-specific ASH/Grb-2 SH3 domain-binding protein (Fragment).												
OS	Bos taurus (Bovine).												
OC	Bukaryota; Metazoa; Chordata; Craniata; Cetartiodactyla; Ruminantia; Bovidae; Bovinae; Bovidae; Bos.												
OC	NCBI_TaxID=9913; RN												
RN	[1]												
SEQUENCE FROM N.A.													
RC	MEDLINE=95230211; PubMed=7174453;												
RA	Qin X.; Waite J.H.; "Exotic collagen gradients in the byssus of the mussel <i>Mytilus edulis".</i>												
RT	J. Exp. Biol. 198:633-644 (1995).												
RL	SEQUENCE 16 AA;												
DR	GO:0004564; F:beta-fructofuranosidase activity; IEA.												
DR	GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.												
DR	GO:00055375; P:carbohydrate metabolism; IEA.												
KW	Glycosidase; Hydrolase.												
FT	NON-TER 1	1	13	13									
FT	NON-TER 13	13 AA;	1541 MW;	1B3053E7384C6874 CRC64;									
SQ	SEQUENCE 13 AA;												
<b>RESULT 9</b>													
Q9TWKL	PRELIMINARY;												
ID	Q9TWKL;	PRT;	16 AA.										
AC	01-MAY-2000 (TREMBLrel. 13, Created)												
RA	Miura K.; Miki H.; Shimazaki K.; Kawai N.; Takenawa T.; "Interaction of ASH/Grb-2 via its SH3 domains with neuron-specific p150 and p65".												
RT	Biochem. J. 316:1639-1645 (1996).												
RL	SEQUENCE 15 AA;												
DR	2516783C74F9CD	CRC64;											
SQ	SEQUENCE 16 AA;												
<b>RESULT 10</b>													
Q9TWKO	PRELIMINARY;												
ID	Q9TWKO;	PRT;	16 AA.										
AC	01-MAY-2000 (TREMBLrel. 13, Created)												
RA	Qin X.; Waite J.H.; "Exotic collagen gradients in the byssus of the mussel <i>Mytilus edulis".</i>												
RT	J. Exp. Biol. 198:633												



OS Zea mays (Maize)  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cy. H98 and cv. C123;  
 RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,  
 RA Morgante M., Rafalski J.A.  
 RT "SNP frequency, haplotype structure and linkage disequilibrium in  
 elite maize inbred lines."  
 RT Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.  
 RL EMBL:AY094452; AAM15707.1;  
 DR EMBL:AY094253; AAM15708.1;  
 FT NON-TER 1 1  
 SQ SEQUENCE 16 AA; 1/20 MN; 02F6CD77295B5610 CRC64;  
 Query Match 24.4%; Score 22; DB 10; Length 16;  
 Best Local Similarity 55.6%; Pred. No. 7e+03;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 7 NAPLGQFP 15  
 : ||| |  
 Db 4 HAPSGFQCP 12

---

RESULT 15  
 P83492 PRELIMINARY; PRT; 7 AA.  
 ID P83492  
 AC P83492;  
 DT 01-JUN-2003 (TREMBLrel. 24, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Alkaline protease Gr3 (EC 3.4.21.-) (Fragment).  
 OS Bionectri ochroleuca (Gliocladium roseum).  
 OC Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Bionectriaceae; Bionectria.  
 OX NCBI\_TAXID=29856;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND SUBCELLULAR LOCATION.  
 RC STRAIN=Gr87;  
 RA Zhao M., Zhang K.;  
 RL Submitted (DEC-2002) to Swiss-Prot.  
 CC -!- FUNCTION: ACTS AS A SERINE PROTEASE.  
 CC -!- SUBCELLULAR LOCATION: SECRETED.  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SB.  
 DR GO:GO-0005576; C:extracellular; NAS.  
 DR GO:0004252; F:serine-type endopeptidase activity; NAS.  
 DR InterPro:IPR0000209; Peptidase S8.  
 DR PROSITE; PS00136; SUBILASE ASP; PARTIAL.  
 DR PROSITE; PS00137; SUBILASE HIS; PARTIAL.  
 DR PROSITE; PS00138; SUBILASE SER; PARTIAL.  
 KW Hydrolase; Serine protease.  
 FT NON-TER 7 7  
 SQ SEQUENCE 7 AA; 688 MN; 776DD455A6C1AD00 CRC64;  
 Query Match 23.3%; Score 21; DB 3; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 SNAP 9  
 : ||| |  
 Db 4 SNAP 7

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on:

June 3, 2004, 15:15:29 ; Search time 53 Seconds  
(without alignments)  
90.628 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_56\_72

Perfect score: 90  
Sequence: 1 QNILLSNAPLGPQFQPF 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04 :\*

- 1: GeneseqP180s:\*
- 2: GeneseqP1990s:\*
- 3: GeneseqP2000s:\*
- 4: GeneseqP2001s:\*
- 5: GeneseqP2002s:\*
- 6: GeneseqP2003as:\*
- 7: GeneseqP2003bs:\*
- 8: GeneseqP2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	79	87.8	15	2	AWI15321	Aaw11321 CLASS II
2	79	87.8	15	2	AWW71591	Aaw71591 CLASS II
3	79	87.8	15	2	AWW85296	Helper T- Aay0209 Amino aci
4	79	87.8	15	2	APY40209	Aay33168 Human Tyr
5	79	87.8	15	2	APY33168	Aay2865 Melanoma- Aay00710 Tumour an
6	79	87.8	15	2	APY26865	Aay49658 Tumour an
7	79	87.8	15	2	APY00710	Aay01748 Exemplary
8	79	87.8	15	2	APY49658	Aay71515 Human Tyr
9	79	87.8	15	2	APY01748	Aab13739 Peptide f
10	79	87.8	15	3	APY71515	Aay9295 Tyrosinas
11	79	87.8	15	3	ABP13739	Aay8291 Tumour as
12	79	87.8	15	3	APY92295	Aay8294 Tyrosinas
13	79	87.8	15	3	APY84291	Aab02617 Tumour as
14	79	87.8	15	3	APY82974	Aab0689 Antigenic
15	79	87.8	15	3	ABP02617	Aam9392 Vaccine r
16	79	87.8	15	3	ABP08689	Aae02106 Tyrosinas
17	79	87.8	15	4	APM99392	Aab31349 Exemplary
18	79	87.8	15	4	ABE02106	Aae0688 Human tyr
19	79	87.8	15	4	ABP31349	Abg7139 Human tyr
20	79	87.8	15	4	APB06836	Aae19078 HLA-DR4 r
21	79	87.8	15	5	ABG7139	Ad19543 Human can
22	79	87.8	15	5	APB19078	Aaw15337 Class II
23	79	87.8	15	6	AD19543	Aam939403 Vaccine r
24	78	86.7	15	2	AWI15337	
25	78	86.7	15	4	AM99401	

## ALIGNMENTS

RESULT 1	ID	AAW15321 standard; peptide; 15 AA.
	XX	AAW15321;
	XX	AC
	XX	DT 09-FEB-1998 (first entry)
	XX	DE
	XX	XX Major histocompatibility complex; MHC; Class II; tyrosinase; vaccine; immune response; immunogenic peptide; melanoma; treatment; protective antibody; immune cells; CD8+ T cell; CD4+ T cell.
	XX	XX Synthetic.
	OS	OS Homo sapiens.
	XX	PN WO9711669-A2.
	PD	PD 03-APR-1997.
	XX	XX 25-SEP-1996; 96WO-US15346.
	XX	PR 26-SEP-1995; 95US-00533895.
	PA	(USSH ) US DEPT HEALTH & HUMAN SERVICES.
	XX	PI Topalian SL, Rosenberg SA, Robbins PF,
	XX	DR WPI: 1997-212652/19.
	XX	PT Major histocompatibility complex Class II immunogenic peptide - used to prevent or treat melanoma in mammal by stimulating production of protective antibodies or immune cells.
	XX	Claim 2; Page 59: 79pp; English.
	CC	Peptides AAW15321-56 are major histocompatibility complex (MHC) Class II restricted melanoma peptides, derived from tyrosinase. Tumour reactive human CD4+ and CD8+ T cells recognise melanoma antigens encoded by the tyrosinase gene. The present sequence is derived from amino acids 56-70. The peptides may be used as a vaccine, either prophylactically in advance of any evidence of melanoma, or therapeutically to enhance the patients own immune response. The immunogenic peptides can be used to prevent or treat melanoma in a mammal by stimulating the production of protective CD4+ T cells, preferably immune cells, or immune cells, or immune positive CD8+ T cells.
	CC	Sequence 15 AA;



Db 1 QNILLSNAPLGQFP 15  
 AAY33168 standard; peptide; 15 AA.  
 RESULT 4  
 AAY40209 ID AAY40209 standard; peptide; 15 AA.  
 XX DT 19-NOV-1999 (first entry)  
 AC AAY40209;  
 XX DE Amino acid sequence of a human melanoma epitope.  
 XX KW Cytotoxic T cell; T lymphocyte; CD8+ epitope; T helper cell;  
 KW CD4+ epitope; B epitope; lipopeptide; interferon gamma; adjuvant;  
 KW vaccine; tumor; infection; immune response; cytokine profile;  
 KW acquired immune deficiency syndrome; papilloma; cancer; hepatitis;  
 KW autoimmune disease.  
 XX OS Homo sapiens.  
 XX PN FR2774687-A1.  
 XX PD 13-AUG-1999.  
 XX PP 06-FEB-1998; 98FR-00001439.  
 XX PR 06-FEB-1998; 98FR-00001439.  
 PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 PA (INSPX ) INST PASTEUR LILLE.  
 XX PS Thiam K, Guillet JC, Ver Waerde C, Auriault C, Gras MH, Loing E;  
 DR WPI; 1999-510734/43.  
 XX PT New lipopeptide comprising C-terminal interferon-gamma fragment with attached lipophilic groups, used as interferon mimic, e.g. for treating cancer or virus infection.  
 PS Disclosure: Page 35; 53pp; French.  
 XX AAY40123-Y40379 represent epitopes that are able to activate cytotoxic T lymphocytes (CD8+ epitopes), T helper cells (CD4+ epitopes), or B cell epitopes recognized by corresponding antibodies. The epitopes may be used in the composition of the invention. The specification describes a lipopeptide that has a peptide part derived from mammalian interferon gamma (IFNG) and one or more lipophilic parts comprising a linear or branched, (un)saturated 4-20C hydrocarbon chain or a steroid. The lipopeptide mimics the activity of IFNG. Compositions comprising the lipopeptides are used to treat or prevent any condition that responds to IFNG, and as adjuvant for vaccines (particularly those directed against tumors, viral or parasitic infections), to stimulate or (re)orient the immune response between types 1 and 2 cytokine profiles. Particular applications are treatment of infections (particularly viral, e.g., acquired immune deficiency syndrome, papilloma (cancer) and hepatitis, but also bacterial, fungal, parasitic or helminth); cancers (particularly of kidney, cutaneous T cells or ovary, chronic myelogenous leukemia or mesothelioma), allergy; and autoimmune diseases  
 XX SQ Sequence 15 AA:  
 Query Match 87.8%; Score 79; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 QNILLSNAPLGQFP 15  
 RESULT 6  
 AAY26865 ID AAY26865 standard; peptide; 15 AA.  
 AC  
 XX  
 RESULT 5





histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte Antigen) that are recognised by T-lymphocytes and elicit an immune response from cytolytic T-lymphocytes (CTL). They function as an immune response stimulator. Tumour rejection antigens are useful in prophylaxis, therapy and diagnosis of tumours and are effective in controlling or preventing tumour growth. The present sequence is the human Tyrosinase peptide-5, that corresponds to residues 56-70 of the tumour associated gene, tyrosinase encoding protein. It can be administered to induce or enhance an immune response and is presented by HLA-DR4 complex. This peptide can serve as a tumour rejection antigen (TRA) and in combination with adjuvants, can produce vaccines useful for treating a variety of tumours.

Sequence 15 AA;

Query Match 87.8%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SQ 1 QNILLSNAPLGQFP 15  
DB 1 QNILLSNAPLGQFP 15

RESULT 11  
AAB13739 standard; peptide; 15 AA.  
XX  
AC AAB13739;  
XX DT 02-FEB-2001 (first entry)  
XX Peptide fragment # 5 from human tyrosinase.  
DE Human; T-cell; immune response; antigen; epitope; B7 family molecule;  
KW Leukocyte function-associated antigen 3; LFA-3.  
KW Intercellular adhesion molecule-1; ICAM-1; vaccine; immunotherapy;  
KW colon polyp; Crohn's disease; ulcerative colitis; breast lesion; tumour;  
KW tyrosinase.  
XX Homo sapiens.  
XX WO200034494-A1.  
XX PD 15-JUN-2000.  
XX PF 12-NOV-1999; 99WO-US026866.  
XX PR 09-DEC-1998; 98US-0111582P.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (THER-) THERION BIOLOGICS CORP.  
XX PI Schlom J, Hodge J, Panicali D;  
XX DR WPI; 2000-431307/37.  
XX PS Claim 18; Page 35; 188pp; English.

Novel recombinant vector useful as immunogens and vaccines for stimulating and enhancing immunological responses to target cells and antigens expresses multiple co-stimulatory molecules such as B7-1, LFA-3, ICAM-1.

PT Novel recombinant vector useful as immunogens and vaccines for stimulating and enhancing immunological responses to target cells and antigens expresses multiple co-stimulatory molecules such as B7-1, LFA-3, ICAM-1.

PT Costimulatory molecules have important roles in T-cell activation and therefore the immune response. The present invention relates to recombinant vector which comprise of foreign nucleic acid sequences encoding at least three costimulatory molecules: a B7 family molecule, Leukocyte function-associated antigen-3 (LFA-3, human CD58) and Intercellular adhesion molecule-1 (ICAM-1, CD54) and optionally a foreign gene encoding a target antigen or immunological epitope. The present sequence is one such target antigen used in the present invention. The present sequence is a tumour-associated antigen. The vector of the

CC present invention would be useful for providing an enhanced immune response to the present target antigen. The vector of the present invention may therefore be useful in immunotherapy for treating or preventing diseases caused by viruses, bacteria, protozoans, parasites, pre-malignant cells and tumour cells. The recombinant vector can be used to treat or prevent preneoplastic or hyperplastic states such as colon polyps, Crohn's disease, ulcerative colitis and breast lesions

SQ Sequence 15 AA;

Query Match 87.8%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQFP 15  
Db 1 QNILLSNAPLGQFP 15

RESULT 12  
AAV92295 standard; peptide; 15 AA.  
ID AAV92295  
XX AC AAV92295;  
XX DT 10-AUG-2000 (first entry)  
DE Tyrosinase antigenic peptide epitope (residues 56-70).  
XX KW Tyrosinase; antigen; epitope; cytotoxic T lymphocyte; CTL; complex;  
KW human leukocyte antigen; HLA.  
XX OS Homo sapiens.  
XX PN WO200020445-A2.  
XX PD 13-APR-2000.  
PP 15-SEP-1999; 99WO-IB001664.  
XX PR 02-OCT-1998; 98US-00165653.  
PR 09-APR-1999; 99US-00289350.  
XX PA (CHAU/) CHAUX P.  
PA (LUIT/) LUITEN R.  
PA (DEMO/) DEMOTTE N.  
PA (DUFF/) DUFFOUR M.  
PA (LURQ/) LURQUIN C.  
PA (TRAV/) TRAVERSARI C.  
PA (STRO/) STROOBANT V.  
PA (CORN/) CORNELIS G R.  
PA (BOON/) BOON-FALLEUR T.  
PA (VBRU/) VAN DER BRUGGEN P.  
PA (SCHU/) SCHULTZ B.  
PA (WARN/) WARNIER G.  
XX PI Chaux P, Luiten R, Demotte N, Dufour M, Lurquin C, Traversari C,  
PI Stroobant V, Cornelis GR, Boon-Fallleur T, Van Der Bruggen P,  
PI Schultz E, Warner G,  
XX DR WPI; 2000-303739/26.

ET Isolation of cytotoxic T-lymphocytes clones by successive steps of stimulation and testing of lymphocytes with antigen presenting cells. Disclosure: Page 22; 99pp; English.

XX A novel method of isolation of cytotoxic T-lymphocytes (CTL) clones comprises successive steps of stimulation and testing of lymphocytes with antigen presenting cells (APCs) which present antigens derived from different expression systems. Disclosure: Page 22; 99pp; English.

CC A novel method of isolation of cytotoxic T-lymphocytes (CTL) clones

CC comprises successive steps of stimulation and testing of lymphocytes with

CC antigen presenting cells (APCs) which present antigens derived from

CC different expression systems. The CTL clones isolated recognize specific

CC antigenic peptides of proteins, preferably of the MAGE family. The APC is

autologous and each expression systems is different from at least one of the other expression systems, therefore isolating a cytotoxic T cell clone specific for the protein. The method can also be used to identify an antigenic peptide epitope. Isolated CTL clones specific for a peptide/human leucocyte antigen (HLA) complex are claimed. The CTL cell lines specific for the complexes, peptides or cells which present the complexes on the cell surface are useful for treating pathological conditions characterized by abnormal expression of the complexes.

SQ Sequence 15 AA;

Query Match 87.8%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQFP 15  
Db 1 QNILLSNAPLGQFP 15

RESULT 13  
AAV84291  
ID AAV84291 standard; Peptide; 15 AA.  
XX  
AC AAY84291;  
XX  
DT 12-JUL-2000 (first entry)  
XX  
DE Tumour associated antigen derived from tyrosinase.  
XX  
KW tumour rejection antigen; macrophage colony stimulating gene;  
KW macrophage-colony stimulating factor; antigen presenting cell;  
KW human leucocyte antigen; CD8+ cytotoxic T lymphocyte.  
XX  
OS Homo sapiens.  
PN WO2000013699-A1.  
XX  
PD 16-MAR-2000.  
XX  
PF 03-SEP-1999; 99WO-US020344.  
XX  
PR 04-SEP-1998; 98US-0099077P.  
PA (LUDW-) LUDWIG INST CANCER RES.

PI Probst-Kepper M, Van Den Eynde B, Boon-Falleur T;  
XX  
DR 2000-256859/22.  
XX  
PT Isolated polypeptide used to treat subjects having a disorder characterized by expression of alternative open reading frame macrophage-colony stimulating factor comprises 25 amino acid residue sequence.  
XX  
PS Disclosure: Page 20: 74pp; English.  
XX  
CC AAY84270-Y84303 represent peptides which are tumour associated antigens. They can be administered in conjunction with the tumour rejection antigen precursor of the invention to induce anti-tumour responses. The tumour rejection antigen precursor of the invention is encoded by an alternative open reading frame (ORF) of human macrophage colony stimulating gene. Peptides derived from the alternative ORF of macrophage-colony stimulating factor, when presented by an antigen presenting cell having a human leucocyte antigen (HLA) class I molecule, effectively induce the activation and proliferation of CD8+ cytotoxic T lymphocytes. Polypeptide and nucleic acids derived from the alternate ORF of macrophage-colony stimulating factor are useful for enriching selectively a population of T lymphocytes with CD8+ T lymphocytes. They are also useful for diagnosing a disorder characterized by expression of the polypeptide, and for identifying functional variants and mimetics

SQ Sequence 15 AA;

Query Match 87.8%; Score 79; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 QNILLSNAPLGQFP 15  
Db 1 QNILLSNAPLGQFP 15

RESULT 14  
AAV84294  
ID AAY82974 standard; peptide; 15 AA.  
XX  
AC AAY82974;  
XX  
DT 19-JUN-2000 (first entry)  
DE Tyrosinase tumour associated antigen.  
XX  
KW Tumour; tumour associated antigen; retrovirus; antisense; treatment;  
KW probe; primer; HLA; cytotoxic T-lymphocyte; cancer; testis; antibody;  
KW CTL; helper T-lymphocyte; MACB; BAGE; GAGE; Grf-V; NUM; CDR4;  
KW beta catenin; tyrosinase; Melan-A; gp100; PRAME.  
XX  
OS Homo sapiens.  
PN WO200006598-A1.  
XX  
PD 10-FEB-2000.  
XX  
PF 15-JUL-1999; 99WO-US016236.  
XX  
PR 29-JUL-1998; 98US-00124398.  
PA (LUDW-) LUDWIG INST CANCER RES.  
XX  
PI Coulie P, Boon-Falleur T;  
DR 2000-205453/18.  
XX  
PT Novel nucleic acids encoding melanoma associated gene products and their fragments and variants, useful for treating endogenous retroviruses.  
XX  
PS Disclosure: Page 26: 77pp; English.  
XX  
CC Tumor associated disorders (e.g. endogenous retrovirus mediated tumors, especially melanomas) can be treated or ameliorated by administering anti sense nucleic acid to reduce the expression of tumour associated genes such as HERV-AVL3-B. Progression of a disorder characterized by the expression of the HERV-AVL3-B endogenous retrovirus tumor rejection antigen (ERTRA) can be diagnosed or monitored by contacting a non-testis biological sample. A disorder can also be treated by administering an agent that enriches the presence of HLA and HERV-AVL3-B ERTRA or by administering autologous cytotoxic T-cells sufficient to ameliorate the disorder. Fragments of the HERV-AVL3-B coding sequence are useful as probes or amplification primers for determining the expression of HERV-AVL3-B genes, to express tumor associated polypeptides in vivo and in vitro and to prepare fragments of such polypeptides to synthesize antibodies. Antigenic peptides of HERV-AVL3-B can be useful for generating antibodies either alone or as fusion proteins, as components of immunoassay and for determining the binding specificity of HLA molecules and/or cytotoxic T lymphocyte (CTL) for HERV-AVL3-B proteins. Peptides derived from the HERV-AVL3-B coding sequence and which are presented by MHC molecules and recognised by CTL or helper T-lymphocytes can be combined with peptides from other tumour rejection antigens by preparation of hybrid nucleic acids or polypeptides to produce polypeptides. This exemplary tumour associated polypeptide corresponds to amino acid 56-70 of the tyrosinase polypeptide. See also AAY82353-Y82986  
SQ Sequence 15 AA;

Query Match 87.8%; Score 79; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 15; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
 Db 1 QNILLSNAPLGQQFP 15

RESULT 15  
 AAB02617

ID AAB02617 standard; peptide, 15 AA.  
 XX

AC AAB02617;

XX DT 1B-AUG-2000 (first entry)

DE Tumour associated peptide antigen from Tyrosinase #6.

XX KW MAGE-A3; HLA class II; human leukocyte antigen; antibody; vaccine;  
 KW cancer; human; tumour; tumour associated gene product.  
 XX OS Homo sapiens.

XX PN WO2000020581-A1.

XX PD 13-APR-2000.

XX PF 15-SEP-1999; 99WO-US021230.

XX PR 05-OCT-1998; 98US-00166448.

XX PA (LUDW-) LUDWIG INST CANCER RES.

PA (UVR-) UNIV VRIJE BRUSSEL.

XX PI Chaux P, Stroobant V, Boon-Falleur T, Van Der Bruggen P;

PI Schulte ES, Van Snick J, Iethé B, Thielemans K, Corthals J;

PI Heirman C;

XX DR 2000-317713/27.

XX PT New MAGE-A3 class II binding peptides, useful to diagnose and treat  
 tumors, are fragments of MAGE-A3 which bind to and are presented to T  
 PT lymphocytes by human leukocyte antigen class II molecules.

XX Disclosure; Page 33; 119pp; English.

XX CC The present invention relates to MAGE-A3 (tumour associated gene product)

CC human leukocyte antigen (HLA) class II-binding peptides (see AAB02566-  
 CC B02595, and AAB02633-B02637). These peptides are presented to T cells in

CC the context of HLA class II molecules. The peptides stimulate the

CC activity and proliferation of CD4+ T lymphocytes. The invention also

CC includes nucleotide sequences encoding MAGE-A3 peptides (see AAA37928 and  
 CC AAA37938-A37940). The peptides and nucleotide sequences can be used to

CC create antibodies against the MAGE-A3 peptides, the antibodies, peptides

CC and nucleotide sequences can be used to create a vaccine. The peptides

CC are used to diagnose or treat a disorder characterized by expression of  
 CC MAGE-3, particularly cancer. The methods can also be used in the

CC diagnosis of disorders associated with MAGE-3 expression. Included in the

CC invention are other human tumour antigens (see AAB02596-B02637), and PCR

CC primers used in the course of the invention (see AAA37929-A37937 and  
 CC AAA37941-A37942)

XX Sequence 15 AA;

Query Match 87.8%; Score 79; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 15; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQQFP 15  
 Db 1 QNILLSNAPLGQQFP 15

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OM protein - protein search, using SW model

Run on: June 3, 2004, 15:26:51 ; Search time 42 Seconds  
(without alignments)  
113,875 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_56\_72  
Perfect score: 90  
Sequence: 1 QNLLSNAPLGPQFPFT 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 206991

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
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 18: /cgnd\_6/picodata/1/pubpaas/us60\_PUBCOMB.pep:  
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	79	87.8	15 9	US-09-923-831-25
2	79	87.8	15 9	US-09-766-89A-37
3	79	87.8	15 12	US-10-218-095-12
4	79	87.8	15 12	US-10-253-286-100
5	79	87.8	15 12	US-10-103-395-198
6	79	87.8	15 14	US-10-161-097-24
7	79	87.8	15 14	US-10-170-832-66
8	79	87.8	15 14	US-10-239-113A-495
9	79	87.8	15 15	US-10-406-317-13
10	79	87.8	15 16	US-10-297-168-13
11	79	87.8	15 16	US-10-239-313A-506
12	78	86.7	15 14	US-10-239-313A-493
13	77	85.6	15 14	US-10-239-313A-497
14	76	84.4	15 14	US-10-239-313A-503
15	76	84.4	15 14	US-10-239-313A-505
16	76	84.4	15 14	US-10-239-313A-481
17	75	83.3	15 14	US-10-239-313A-492
18	75	83.3	15 14	US-10-239-313A-494
19	75	83.3	15 14	US-10-239-313A-500
20	75	81.1	15 14	US-10-239-313A-496
21	73	81.1	15 14	US-10-239-313A-502
22	73	81.1	15 14	US-10-239-313A-504
23	73	78.9	15 14	US-10-239-313A-498
24	71	78.9	15 14	US-10-239-313A-499
25	70	77.3	13 9	US-09-847-185-41
26	66	73.3	13 9	US-10-219-850-21
27	66	73.3	13 9	US-10-353-678-27
28	43	47.8	9 14	US-10-24-86-41
29	43	36.7	14 10	US-09-880-748-2371
30	33	36.7	14 10	US-09-880-748-615
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32	33	36.7	14 12	US-10-193-412-2615
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34	32	35.6	13 14	US-09-880-748-5603
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36	32	35.6	14 10	US-10-23-418-2603
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38	32	35.6	14 14	US-10-224-999A-3225
39	32	35.6	15 14	US-10-24-999A-3235
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41	32	35.6	15 14	US-10-24-999A-3237
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43	32	35.6	16 14	US-10-24-999A-3248
44	32	35.6	16 14	US-10-24-999A-3249
45	32	35.6	16 14	US-10-24-999A-3250

## ALIGNMENTS

RESULT 1  
US-09-923-831-25  
; Sequence 25, Application US/09923831  
; Patent No. US20020115142A1  
; GENERAL INFORMATION:  
; APPLICANT: Martelange, Val, rie  
; De Smet, Charles  
; APPLICANT: Boon-Falleur, Thierry  
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
; FILE REFERENCE: L0461/7054  
; CURRENT APPLICATION NUMBER: US/09/923, 831  
; PRIOR FILING DATE: 2001-08-07  
; PRIOR APPLICATION NUMBER: 09/183, 706  
; PRIORITY FILING DATE: 2001-10-30  
; SEQ ID NO: 43  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-923-831-25

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	79	87.8	15 9	Sequence 25, Appl
2	79	87.8	15 9	Sequence 37, Appl
3	79	87.8	15 12	Sequence 32, Appl
4	79	87.8	15 12	Sequence 500, Appl
5	79	87.8	15 12	Sequence 198, Appl
6	79	87.8	15 14	Sequence 24, Appl
7	79	87.8	15 14	Sequence 66, Appl
8	79	87.8	15 14	Sequence 495, Appl
9	79	87.8	15 12	Sequence 32, Appl
10	79	87.8	15 15	Sequence 13, Appl
11	79	87.8	15 16	Sequence 13, Appl
12	78	86.7	15 14	Sequence 506, Appl
13	77	85.6	15 14	Sequence 493, Appl
14	76	84.4	15 14	Sequence 497, Appl
15	76	84.4	15 14	Sequence 503, Appl

RESULT 2  
US-09-766-889A-37  
; Sequence 25, Application US/09766889A  
; Patent No. US200201465A1  
; GENERAL INFORMATION:  
; APPLICANT: Luitjen, Rosalie  
; APPLICANT: Boon-Falleur, Thierry  
; APPLICANT: van der Bruggen, Pierre

APPLICANT: Stroobant, Vincent  
 APPLICANT: Demotte, Nathalie  
 APPLICANT: Schultz, Erwin  
 TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44  
 FILE REFERENCE: L00461-7104  
 CURRENT APPLICATION NUMBER: US/09/766, 889A  
 CURRENT FILING DATE: 2001-01-19  
 PRIOR APPLICATION NUMBER: US 60/177, 242  
 PRIOR FILING DATE: 2000-01-20  
 PRIOR APPLICATION NUMBER: US 60/243, 212  
 PRIOR FILING DATE: 2000-10-25  
 NUMBER OF SEQ ID NOS: 59  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 37  
 ORGANISM: Homo sapiens  
 US-09-766-889A-37

Query Match 87.8%; Score 79; DB 9; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
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Qy 1 QNILLSNAPLGQFP 15

Dy 1 QNILLSNAPLGQFP 15

RESULT 3  
 US-10-218-095-32  
 Sequence 32, Application US/10218095  
 Publication No. US20040033541A1  
 GENERAL INFORMATION:  
 APPLICANT: Zhang, Yi  
 APPLICANT: Stroobant, Vincent  
 APPLICANT: Russo, Vincenzo  
 APPLICANT: Boon-Falleure, Thierry  
 APPLICANT: van der Bruggen, Pierre  
 TITLE OF INVENTION: MAGE-A4 ANTIGENIC PEPTIDES AND USES THEREOF  
 FILE REFERENCE: L00461-70137  
 CURRENT APPLICATION NUMBER: US/10/218, 095  
 CURRENT FILING DATE: 2002-08-13  
 NUMBER OF SEQ ID NOS: 63  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 32  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-218-095-32

Query Match 87.8%; Score 79; DB 12; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQFP 15

Dy 1 QNILLSNAPLGQFP 15

RESULT 4  
 US-10-253-286-500  
 Sequence 500, Application US/10253286  
 Publication No. US20040058881A1  
 GENERAL INFORMATION:  
 APPLICANT: HUMPHREYS, ROBERT  
 APPLICANT: XU, MINZHEN  
 TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
 FILE REFERENCE: REB-2015  
 CURRENT APPLICATION NUMBER: US/10/253, 286  
 CURRENT FILING DATE: 2003-11-13  
 PRIOR APPLICATION NUMBER: 10/197, 000  
 PRIOR FILING DATE: 2002-07-17  
 PRIOR APPLICATION NUMBER: 09/395, 813

Query Match 87.8%; Score 79; DB 12; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQFP 15

Dy 1 QNILLSNAPLGQFP 15

RESULT 5  
 US-10-103-395-198  
 Sequence 198, Application US/10103395  
 Publication No. US20020160019A1  
 GENERAL INFORMATION:  
 APPLICANT: EPIMUNE, Inc.  
 APPLICANT: Sette, Alessandro  
 APPLICANT: Sidney, John  
 APPLICANT: Southwood, Scott  
 TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR  
 TITLE OF INVENTION: RESTRICTED EPITOPES  
 FILE REFERENCE: 39963-20016.01  
 CURRENT APPLICATION NUMBER: US/10/103, 395  
 CURRENT FILING DATE: 2003-01-03  
 PRIOR APPLICATION NUMBER: US 09/009, 953  
 PRIOR APPLICATION NUMBER: 1998-01-21  
 PRIOR APPLICATION NUMBER: PCT/US98/01373  
 PRIOR APPLICATION NUMBER: 1998-01-23  
 PRIOR APPLICATION NUMBER: US 60/036, 713  
 PRIOR APPLICATION NUMBER: 1997-01-23  
 PRIOR APPLICATION NUMBER: US 60/037, 432  
 PRIOR FILING DATE: 1997-02-07  
 NUMBER OF SEQ ID NOS: 274  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 198  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-103-395-198

Query Match 87.8%; Score 79; DB 12; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQFP 15

Dy 1 QNILLSNAPLGQFP 15

RESULT 6  
 US-10-161-097-24  
 Sequence 24, Application US/10161097  
 Publication No. US2003009404A1  
 GENERAL INFORMATION:  
 APPLICANT: ROSENZWEIG, Michael  
 APPLICANT: PYKETT, Mark J.  
 APPLICANT: SCADDEN, David T.  
 APPLICANT: POZNANSKY, Mark C.  
 TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION  
 TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL  
 TITLE OF INVENTION: DEVICES  
 FILE REFERENCE: C1005/7012/KA/ERG  
 CURRENT APPLICATION NUMBER: US/10/161, 097  
 CURRENT FILING DATE: 2002-05-31  
 PRIOR APPLICATION NUMBER: US/09/574, 749

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; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/107,972
; CURRENT FILING DATE: 1998-11-12
; CURRENT APPLICATION NUMBER: US/10/239,313A
; PRIORITY NUMBER: PCT/US99/26795
; PRIORITY NUMBER: 2002-09-19
; PRIORITY NUMBER: FR 00/03711
; PRIORITY NUMBER: 2000-03-23
; PRIORITY NUMBER: PCT 01/70772
; PRIORITY NUMBER: 2001-03-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 24
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Homo Sapiens source
US-10-161-097-24

Query Match 87.8%; Score 79; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQFP 15
Db 1 QNILLSNAPLGQFP 15

RESULT 7
US-10-170-832-66
Sequence 66, Application US/10170832
Publication No. US20030170792A1
GENERAL INFORMATION:
APPLICANT: Chaux, Pascal
APPLICANT: Vantonne, Valrie
APPLICANT: Stroobant, Vincent
APPLICANT: Boon-Palleur, Thierry
APPLICANT: van der Bruggen, Pierre
APPLICANT: Thielmans, Kris
APPLICANT: Corthals, Jurgen
TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
FILE REFERENCE: L04617/052
CURRENT APPLICATION NUMBER: US/10/170,832
CURRENT FILING DATE: 2002-06-12
PRIORITY NUMBER: US/09/166,448
PRIOR FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 66
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
US-10-170-832-66

Query Match 87.8%; Score 79; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNILLSNAPLGQFP 15
Db 1 QNILLSNAPLGQFP 15

RESULT 8
US-10-239-313A-495
Sequence 495, Application US/10239313A
Publication No. US2003017525A1
GENERAL INFORMATION:
APPLICANT: KLINGNER - HAMOUR, Christine
APPLICANT: CORVIA, Nathalie
APPLICANT: BECK, Alain
APPLICANT: GOETSCH, Liliane
TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 38163-0189
; TITLE OF INVENTION: molecules and uses thereof
; CURRENT APPLICATION NUMBER: US/10/406,317
; CURRENT FILING DATE: 2003-04-04
; PRIORITY NUMBER: US/09/856,988
; PRIORITY NUMBER: PCT/US99/26866
; PRIORITY NUMBER: 2001-05-30
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; PRIORITY NUMBER: 1999-11-12

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; PRIORITY APPLICATION NUMBER: 60/111,582
; PRIOR FILING DATE: 1998-12-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 13
; LENGTH: 15
; TYPE: PRT
; FEATURE: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-10-406-317-13

Query Match 87.8%; Score 79; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Organism: Homo sapiens

Qy 1 QNILLSNAPLGQFP 15
Db 1 QNILLSNAPLGQFP 15

RESULT 12
US-10-239-213A-506
; Sequence 506, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; CORVATA, Nathalie
; BECK, Alain
; GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/0772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SEQ ID NO 493
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-213A-506

Query Match 87.8%; Score 79; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Organism: Homo sapiens
US-10-297-168-13

Qy 1 QNILLSNAPLGQFP 15
Db 1 QNILLSNAPLGQFP 15

RESULT 13
US-10-239-313A-493
; Sequence 493, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; CORVATA, Nathalie
; BECK, Alain
; GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/0772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SEQ ID NO 493
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-493

Query Match 86.7%; Score 78; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.9e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Organism: Homo sapiens

Qy 1 QNILLSNAPLGQFP 15
Db 1 QNILLSNAPLGQFP 15

RESULT 14
US-10-239-313A-497
; Sequence 497, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; CORVATA, Nathalie
; BECK, Alain
; GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/0772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SEQ ID NO 493
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-497

Query Match 85.6%; Score 77; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.8e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Organism: Homo sapiens
US-10-239-313A-497

Qy 1 QNILLSNAPLGQFP 15
Db 1 QNILLSNAPLGQFP 15

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; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SEQ ID NO: 497
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-97

Query Match          Score 76; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.9e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db      1 QNILLSNAPVGQQFP 15

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RESULT 15
US-10-239-313A-503
Sequence 503, Application US/10249313A
Publication No. US20030175285A1
GENERAL INFORMATION:
; APPLICANT: XLINGUER - HAMOUR, Christine
; APPLICANT: CORVATA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SEQ ID NO: 503
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-503

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Query Match          Score 76; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.9e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy      1 QNILLSNAPLGQQFP 15
Db      1 QNILLSNAPGQQFP 15

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Search completed: June 3, 2004, 15:32:22  
Job time : 42 secs

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## OM Protein - protein search, using sw model

Run on: June 3, 2004, 15:24:30 ; Search time 23 Seconds

(without alignments)  
38.158 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_56\_72

Perfect score: 90  
Sequence: 1 QNILLISNAPLGPRQFDTT 17

Scoring table: BLOSUM62  
Gapext: 0.5

Searched:

389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/pctodata/2/iaa/5A COMB.pep:  
2: /cgn2\_6/pctodata/2/iaa/5B COMB.pep:  
3: /cgn2\_6/pctodata/2/iaa/6A COMB.pep:  
4: /cgn2\_6/pctodata/2/iaa/6B COMB.pep:  
5: /cgn2\_6/pctodata/2/iaa/6C COMB.pep:  
6: /cgn2\_6/pctodata/2/iaa/PCUTS COMB.pep:  
\* /cgn2\_6/pctodata/2/iaa/backfiles1.pep:  
\* /cgn2\_6/pctodata/2/iaa/backfiles1.pep:  
\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	87.8	15	2	US-09-036-582-22
2	79	87.8	15	3	US-09-183-706-25
3	79	87.8	15	3	US-09-166-448-66
4	79	87.8	15	4	US-09-567-955-25
5	79	87.8	15	4	US-09-165-863-22
6	79	87.8	15	4	US-09-093-198
7	79	87.8	15	4	US-09-697-884-66
8	79	87.8	15	4	US-09-289-350-22
9	79	87.8	15	4	US-09-574-749B-24
10	79	87.8	15	4	US-09-318-141-22
11	79	87.8	15	4	US-09-601-712
12	80.0	80.0	15	4	US-09-169-717E-28
13	66	73.3	13	2	US-08-902-516-41
14	66	73.3	13	4	US-09-847-184-41
15	33	36.7	9	3	US-08-159-339A-783
16	33	36.7	10	3	US-08-159-339A-747
17	31	34.4	9	2	US-08-725-73D-13
18	31	34.4	9	3	US-09-162-368B-13
19	31	34.4	9	3	US-09-161-87B-13
20	31	34.4	9	4	US-09-311-784A-402
21	31	34.4	10	1	US-08-461-005-1
22	31	34.4	10	2	US-07-930-685-1
23	30	33.3	9	4	US-09-311-784A-411
24	30	33.3	15	3	US-08-787-091-4
25	30	33.3	16	3	US-08-787-091-16
26	30	33.3	16	4	US-09-461-325-515
27	30	33.3	16	4	US-10-012-542-515

## ALIGNMENTS

```
RESULT 1
US-09-036-582-22
; Sequence 22, Application US/09036582A
; Patent No. 5965381
; GENERAL INFORMATION:
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Cornelis, Guy R.
; TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EURARYOTIC CELLS
; TITLE OF INVENTION: WITH RECOMBINANT YERSINIA
; FILE REFERENCE: 11154
; CURRENT APPLICATION NUMBER: US/09/036,582A
; CURRENT FILING DATE: 09/03/06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 22
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human Tyrosinase peptide
US-09-036-582-22
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Query Match 67.8%
Best Local Similarity 100.0%
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 QNILLISNAPLGPOFP 15
Db 1 QNILLISNAPLGPOFP 15
Query Match 67.8%
Best Local Similarity 100.0%
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 QNILLISNAPLGPOFP 15
Db 1 QNILLISNAPLGPOFP 15
RESULT 2
US-09-183-706-25
; Sequence 25, Application US/09183706
; Patent No. 6245325
; GENERAL INFORMATION:
; APPLICANT: Martelange, Valrie
; APPLICANT: De Smet, Charles
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: 10461/7054
; CURRENT APPLICATION NUMBER: US/09/183,706
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 09/122,989
; EARLIER FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 43
; SEQ ID NO: 25
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-183-706-25
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Query Match      87.8%; Score 79; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QNILLSNAPLGQQFP 15  
 Db      1 QNILLSNAPLGQQFP 15

RESULT 3

US-09-166-448-66  
 ; Sequence 66, Application US/09166448  
 ; Patent No. 6291430  
 ; GENERAL INFORMATION:  
 ;   APPLICANT: Chaux, Pascal  
 ;   APPLICANT: Vantomme, Valrie  
 ;   APPLICANT: Stroobant, Vincent  
 ;   APPLICANT: Boon-Falleur, Thierry  
 ;   APPLICANT: van der Bruggen, Pierre  
 ;   APPLICANT: Thielemans, Kris  
 ;   APPLICANT: Corthals, Jurgen  
 ; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
 ; FILE REFERENCE: L0461/7052  
 ; CURRENT APPLICATION NUMBER: US/09/166,448  
 ; CURRENT FILING DATE: 1998-10-05  
 ; NUMBER OF SEQ ID NOS: 81  
 ; SOFTWARE: FASTSEQ for Windows Version 3.0  
 ; SEQ ID NO: 66  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-166-448-66

Query Match      87.8%; Score 79; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QNILLSNAPLGQQFP 15  
 Db      1 QNILLSNAPLGQQFP 15

RESULT 4

US-09-567-995-25  
 ; Sequence 25, Application US/09567995  
 ; Patent No. 6203756  
 ; GENERAL INFORMATION:  
 ;   APPLICANT: Martelange, Valerie  
 ;   APPLICANT: De Smet, Charles  
 ;   APPLICANT: Boon-Falleur, Thierry  
 ; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
 ; FILE REFERENCE: L0461/7054  
 ; CURRENT APPLICATION NUMBER: US/09/567,995  
 ; CURRENT FILING DATE: 2000-05-10  
 ; PRIOR APPLICATION NUMBER: 09/183,706  
 ; PRIOR FILING DATE: 1998-10-30  
 ; NUMBER OF SEQ ID NOS: 43  
 ; SEQ ID NO: 25  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-567-995-25

Query Match      87.8%; Score 79; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QNILLSNAPLGQQFP 15  
 Db      1 QNILLSNAPLGQQFP 15

RESULT 5

US-09-165-863-22  
 ; Sequence 22, Application US/09165863  
 ; Patent No. 6407063  
 ; GENERAL INFORMATION:  
 ;   APPLICANT: Luitin, Rosalie  
 ;   APPLICANT: Durfour, Nathalie  
 ;   APPLICANT: van der Bruggen, Pierre  
 ;   APPLICANT: Cornelis, Guy  
 ;   APPLICANT: Stroobant, Vincent  
 ;   APPLICANT: Lurquin, Christophe  
 ;   APPLICANT: Boon-Falleur, Thierry  
 ;   APPLICANT: Chaux, Pascal  
 ; TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL  
 ;   PROCEDURE  
 ; FILE REFERENCE: L11727  
 ; CURRENT APPLICATION NUMBER: US/09/165,863  
 ; CURRENT FILING DATE: 1999-10-02  
 ; NUMBER OF SEQ ID NOS: 45  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 22  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Human Tyrosinase peptide  
 US-09-165-863-22

Query Match      87.8%; Score 79; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QNILLSNAPLGQQFP 15  
 Db      1 QNILLSNAPLGQQFP 15

RESULT 6

US-09-009-953-198  
 ; Sequence 198, Application US/09009953  
 ; Patient No. 6413517  
 ; GENERAL INFORMATION:  
 ;   APPLICANT: Sette, Alessandro  
 ; TITLE OF INVENTION: Identification of Broadly  
 ;   Reacting DR Restricted Epitopes  
 ; NUMBER OF SEQUENCES: 274  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, Eighth Floor  
 ; CITY: San Francisco  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94111-3834  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: PAUSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/009,953  
 ; FILING DATE: 21-Jan-1998  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/036,713  
 ; FILING DATE: 23-JAN-1997  
 ; APPLICATION NUMBER: US 60/037,432  
 ; FILING DATE: 07-FEB-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Weber, Ellen Lauver  
 ; REGISTRATION NUMBER: 32,762  
 ; REFERENCE/DOCKET NUMBER: 018623-011520US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-576-0200  
 ; TELEFAX: 415-576-0300  
 ; TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 198:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 MOLECULE TYPE: linear  
 PEPTIDE DESCRIPTION: SEQ ID NO: 198:  
 US-09-009-953-198

Query Match Score 87.8%; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 QNILLSNAPLGQFP 15	Qy	1 QNILLSNAPLGQFP 15
Db	1 QNILLSNAPLGQFP 15	Db	1 QNILLSNAPLGQFP 15

RESULT 7  
 Sequence 66, Application US/09697894  
 Patent No. 642817  
 GENERAL INFORMATION:  
 APPLICANT: Chaux, Pascal  
 APPLICANT: Vantomme, Valérie  
 APPLICANT: Stroobant, Vincent  
 APPLICANT: Boon-Falleur, Thierry  
 APPLICANT: van der Bruggen, Pierre  
 APPLICANT: Thielemans, Kris  
 TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
 FILE REFERENCE: L0461/T052  
 CURRENT APPLICATION NUMBER: US/09/697,884  
 CURRENT FILING DATE: 2000-10-27  
 PRIOR APPLICATION NUMBER: 09/166,448  
 PRIOR FILING DATE: 1998-10-05  
 NUMBER OF SEQ ID NOS: 81  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 66  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-697-884-66

Query Match Score 87.8%; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 QNILLSNAPLGQFP 15	Qy	1 QNILLSNAPLGQFP 15
Db	1 QNILLSNAPLGQFP 15	Db	1 QNILLSNAPLGQFP 15

RESULT 8  
 Sequence 22, Application US/09289350  
 Patent No. 6531451  
 GENERAL INFORMATION:  
 APPLICANT: Chaux, Pascal  
 APPLICANT: Luiten, Rosalie  
 APPLICANT: Demotte, Nathalie  
 APPLICANT: Deffour, Marie-Therese  
 APPLICANT: Lurquin, Christophe  
 APPLICANT: Traversari, Catin  
 APPLICANT: Stroobant, Vincent  
 APPLICANT: Cornelis, Guy R.  
 APPLICANT: Van Der Bruggen, Pierre  
 TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL PROCEDURE  
 FILE REFERENCE: 117272  
 CURRENT APPLICATION NUMBER: US/09/289,350

INFORMATION FOR SEQ ID NO: 199:  
 CURRENT FILING DATE: 1999-04-09  
 PRIOR APPLICATION NUMBER: 09/165,863  
 PRIOR FILING DATE: 1998-10-02  
 NUMBER OF SEQ ID NOS: 49  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 22  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Human Tyrosinase peptide  
 US-09-289-350-22

RESULT 9  
 Sequence 24, Application US/09574749B  
 Patent No. 6548299  
 GENERAL INFORMATION:  
 APPLICANT: ROSENWEIG, Michael  
 APPLICANT: PYKETT, Mark J.  
 APPLICANT: SCADDEN, David T.  
 APPLICANT: POZNANSKY, Mark C.  
 TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION  
 TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL  
 TITLE OF INVENTION: DEVICES  
 FILE REFERENCE: C10005/T012/KA/ERG  
 CURRENT APPLICATION NUMBER: US/09/574,749B  
 CURRENT FILING DATE: 2002-05-31  
 PRIOR APPLICATION NUMBER: US 60/107,972  
 PRIOR FILING DATE: 1998-11-12  
 PRIOR APPLICATION NUMBER: PCT/US99/26795  
 PRIOR FILING DATE: 1999-11-12  
 PRIOR APPLICATION NUMBER: US 09/524,749  
 NUMBER OF SEQ ID NOS: 58  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 24  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Homo Sapiens source  
 US-09-574-749B-24

RESULT 10  
 Sequence 22, Application US/09318141  
 Patent No. 6602506  
 GENERAL INFORMATION:  
 APPLICANT: van der Bruggen, Pierre  
 APPLICANT: Cornelis, Guy R.  
 TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS  
 FILE REFERENCE: 11154  
 CURRENT APPLICATION NUMBER: US/09/318,141  
 CURRENT FILING DATE: 1999-05-25  
 EARLIER APPLICATION NUMBER: US 09/036,582

; CURRENT FILING DATE: 1998-03-06  
 ; NUMBER OF SEQ ID NOS: 39  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 22  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Human Tyrosinase peptide  
 US-09-318-141-22  
 ; US-09-169-717E-28

Query Match	Score 79;	DB 4;	Length 15;	
Best Local Similarity	100.0%;	Pred. No.	9.4e-07;	
Matches	0;	Mismatches	0;	Indels
Qy	1 QNILLSNAPLGQFP 15			0;
Db	1 QNILLSNAPLGQFP 15			

RESULT 11  
 US-09-601-729-112 Application US/09601729  
 ; Patent No. 6683052  
 ; GENERAL INFORMATION:  
 ; APPLICANT: THIAMI, KADER  
 ; APPLICANT: AURIAULT, CLAUDE  
 ; APPLICANT: GRAS-MASSE, HELENE  
 ; APPLICANT: LOING, ESTELLE  
 ; APPLICANT: VERWAERDE, CLAUDIE  
 ; APPLICANT: GUILLET, JEAN GERARD  
 ; TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES  
 ; FILE REFERENCE: USB-97-AU-IN  
 ; CURRENT APPLICATION NUMBER: US/09/601,729  
 ; PRIOR APPLICATION NUMBER: PCT/FR99/00259  
 ; PRIOR FILING DATE: 1999-02-05  
 ; PRIOR APPLICATION NUMBER: 98 01439  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 281  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 112  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: peptide  
 US-09-601-729-112

Query Match	Score 79;	DB 4;	Length 15;	
Best Local Similarity	100.0%;	Pred. No.	9.4e-07;	
Matches	0;	Mismatches	0;	Indels
Qy	1 QNILLSNAPLGQFP 15			0;
Db	1 QNILLSNAPLGQFP 15			

RESULT 12  
 US-09-169-717E-28 Application US/09169717E  
 ; Patent No. 6667037  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Doms, Annie  
 ; APPLICANT: Degiovanni, Gerard  
 ; APPLICANT: Morel, Sandra  
 ; APPLICANT: Van den Eynde, Benoit  
 ; APPLICANT: Boon-Palleur, Thierry  
 ; TITLE OF INVENTION: Isolator Peptides Which Bind To HLA-B35 Molecules,  
 ; TITLE OF INVENTION: Larger Peptides Which Contain These, Nucleic Acid  
 ; FILE REFERENCE: LUD551  
 ; CURRENT APPLICATION NUMBER: US/09/169,717E

; CURRENT FILING DATE: 1998-10-09  
 ; NUMBER OF SEQ ID NOS: 39  
 ; SEQ ID NO: 28  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 US-09-169-717E-28

Query Match	Score 80.0%;	DB 4;	Length 15;	
Best Local Similarity	93.3%;	Pred. No.	1.3e-05;	
Matches	14;	Conservative	0;	Mismatches
Qy	1 QNILLSNAPLGQFP 15			0;
Db	1 QNILLSNAPLGQFP 15			

RESULT 13  
 US-08-902-516-41 Application US/08902516  
 ; Patent No. 5851432  
 ; Segenice 41; Application US/08902516  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SOO HOO, William  
 ; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
 ; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
 ; RESPONSE USING SAME  
 ; TITLE OF INVENTION: COMBINING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
 ; NUMBER OF SEQUENCES: 50  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CAMPBELL & FLORES, LLP  
 ; STREET: 4370 La Jolla Village Drive, Suite 700  
 ; CITY: San Diego  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 92121  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatientIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/902,516  
 ; FILING DATE: 29-JUL-1997  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Campbell, Kathryn A.  
 ; REGISTRATION NUMBER: 31,315  
 ; REFERENCE/DOCKET NUMBER: P-IM 24442  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (619)335-9001  
 ; TELEFAX: (619)335-8949  
 ; INFORMATION FOR SEQ ID NO: 41:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 13 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: Peptide  
 US-08-902-516-41

Query Match	Score 73.3%;	DB 2;	Length 13;	
Best Local Similarity	100.0%;	Pred. No.	0.00011;	
Matches	13;	Conservative	0;	Mismatches
Qy	1 QNILLSNAPLGQ 13			0;
Db	1 QNILLSNAPLGQ 13			

RESULT 14  
 US-09-847-1185-41 Application US/09847185  
 ; Sequence 41; Application US/09847185  
 ; Patent No. 6482207  
 ; GENERAL INFORMATION:

APPLICANT: Soo Hoo, William  
 TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
 NUMBER OF SEQUENCES: 50  
 RESPONSE USING SAME  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CAMPBELL & FLORES, LLP  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: United States  
 ZIP: 92121  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 CURRENT APPLICATION DATA: Patent In Release #1.0, Version #1.25  
 FILING DATE: 01-MAY-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/201, 931  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Catherine A.  
 REGISTRATION NUMBER: 31, 815  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9001  
 TELEFAX: (619) 535-8949  
 INFORMATION FOR SEQ ID NO: 41:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 41:

US-09-847-185-41

Query Match 73.3%; Score 66; DB 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.00011;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ONTILLISNAPIGPQ 13  
 Db 1 ONTILLISNAPIGPQ 13

RESULT 15  
 US-08-159-339A-783  
 Sequence 783; Application US/08159339A  
 Patent No. 6037135  
 GENERAL INFORMATION:  
 APPLICANT: Kubo, Ralph T.  
 APPLICANT: Grey, Howard M.  
 APPLICANT: Sette, Alessandro  
 APPLICANT: Celis, Esteban  
 TITLE OF INVENTION: HLA Binding peptides and Their  
 NUMBER OF SEQUENCES: 1254  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/159, 339A  
 FILING DATE: 29-NOV-1993  
 CLASSIFICATION: 424  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/926, 666  
 FILING DATE: 07-AUG-1992  
 APPLICATION NUMBER: US 08/027, 746  
 FILING DATE: 05-MAR-1993  
 APPLICATION NUMBER: US 08/103, 396  
 FILING DATE: 06-AUG-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Weber, Ellen Lauver  
 REGISTRATION NUMBER: 32, 752  
 REFERENCE/DOCKET NUMBER: 018623-005030US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 783:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-159-339A-783

Query Match 36.7%; Score 33; DB 3;  
 Best Local Similarity 85.7%; Pred. No. 3e+05;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 PLGPQGP 15  
 |||||  
 Db 2 PLGPQGP 8

Search completed: June 3, 2004, 15:27:52  
 Job time : 23 secs  
 Job time : 23 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: June 3, 2004, 15:09:24 ; Search time 13.5 Seconds

Title: US-08-533-895A-39\_COPY\_448\_462  
 Perfect score: 83  
 Sequence: 1 DSYLQSDPDSFQD 15

Scoring table: BLOSUM62

Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%

Listing first 45 summaries

Database : PIR;78:+

- 1: Pir1\*
- 2: Pir2\*
- 3: Pir3\*
- 4: Pir4\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	83	100.0	529 YRHUI	monophenol monooxygenase (EC 1.14.18.1) precursor [validated] - human
2	54	65.1	533 YRMSCS	monophenol monooxygenase (EC 1.14.18.1) precursor [validated] - human
3	49	59.0	336 A69416	monophenol monooxygenase (EC 1.14.18.1) precursor [validated] - human
4	45	54.2	274 JW0077	pyruvate formate-1-chitinate (EC 3.2.1.1)
5	45	54.2	393 AC1142	N-acetyl-L-amino acid
6	45	54.2	393 AF1500	N-acetyl-L-amino acid
7	45	54.2	476 C94687	probable fatty acyl
8	43	51.8	150 T38629	hypothetical prote
9	43	51.8	620 S56790	probable membrane
10	43	51.8	1093 H84126	cation efflux syst
11	43	51.8	1744 AH0972	tansabin - African
12	42.5	51.2	862 T24974	lipoxigenase (EC 3.4.13.12)
13	41	49.4	517 F71417	cytochrome P450 -
14	41	49.4	561 D7034	oligo-1,6-glucosidase
15	40	48.2	184 ZRBPT9	gene 3 protein -
16	40	48.2	295 S29045	estrene sulfotrans
17	40	48.2	337 AH0972	lipopolysaccharide
18	40	48.2	368 T24974	hypothetical prote
19	40	48.2	550 HYSMCA	mycolysin (EC 3.4.13.12)
20	40	48.2	585 S06958	spingomyelin phos
21	40	48.2	596 S30973	minor tail protein
22	40	48.2	629 A39825	spingomyelin phos
23	40	48.2	638 A30347	exotoxin A precurs
24	40	48.2	638 C83503	exotoxin A precurs
25	40	48.2	901 C83427	probable transcrip
26	40	48.2	940 T01854	hypothetical prote
27	39	47.0	130 B82589	hypothetical prote
28	39	47.0	185 T15399	hypothetical prote
29	39	47.0	239 G97829	tRNA nucleotidylyl

## ALIGNMENTS

RESULT 1

YRHUI

monophenol monooxygenase (EC 1.14.18.1) precursor [validated] - human  
 NI:Alternate names: cresolase; monophenol oxidase; phenolase; tyrosinase  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Jun-1990 #Sequence revision 31-Mar-1993 #Text change 08-Dec-2000  
 C:Accession: A38444; S07760; A33333; A38718; A40598; S04760; A60149; B60149; S53  
 R;Giebel, L.B.; Strunk, K.M.; Spritz, R.A.  
 Genomics 9 435-445, 1991  
 A;Title: Organization and nucleotide sequences of the human tyrosinase gene and a truncated  
 A;Reference number: A38444; MUID:91236163; PMID:1903356  
 A;Accession: A38444  
 A;Molecule type: DNA  
 A;Residues: 1-529 <KIK>  
 A;Cross-References: EMBL:XI6073; PID:CA34205.1; PID:937507  
 R;Takeda, A.; Tomita, Y.; Okinaga, S.; Tagami, H.; Shibahara, S.  
 Biochim. Biophys. Acta 1009, 283-286, 1989  
 A;Title: Characteristic sequences in the upstream region of the human tyrosinase gene.  
 A;Reference number: S07760; MUID:9089403; PMID:2480811  
 A;Accession: A33333  
 A;Molecule type: DNA  
 A;Residues: 1-273 <KIK>  
 A;Cross-References: EMBL:XI6073; PID:CA34205.1; PID:937507  
 R;Takeda, A.; Tomita, Y.; Okinaga, S.; Tagami, H.; Shibahara, S.  
 Biochim. Biophys. Res. Commun. 162, 984-980, 1989  
 A;Title: Functional analysis of the cDNA encoding human tyrosinase precursor.  
 A;Reference number: A33333; MUID:89351001; PMID:2504160  
 A;Accession: A33333  
 A;Molecule type: DNA  
 A;Residues: 1-32 <KIK>  
 A;Cross-References: GB:M27160  
 R;Giebel, L.B.; Tripathi, R.B.; Strunk, K.M.; Jackson, C.E.; King, R.A.;  
 Am. J. Hum. Genet. 48, 1159-1167, 1991  
 J. Exp. Med. 169, 2029-2042, 1999  
 A;Title: Tyrosinase gene mutations associated with type IB ("Yellow") oculocutaneous albinism  
 A;Reference number: A38718; MUID:91241133; PMID:1903591  
 A;Accession: A38718  
 A;Molecule type: DNA  
 A;Residues: 1-380 <GR>  
 R;Bouchard, B.; Fuller, B.B.; Vijayasaradhi, S.; Houghton, A.N.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 5272-5276, 1991  
 A;Title: Induction of pigmentmentation in mouse fibroblasts by expression of human tyrosinase  
 A;Reference number: J00098; MUID:89229151; PMID:2493655  
 A;Accession: J00098  
 A;Molecule type: mRNA  
 A;Residues: 1-178 'I', 180-191 'Y', 191-529 <BOU>  
 R;Chintamani, C.D.; Halabian, R.; Kobayashi, Y.; Witkop Jr., C.J.; Kwon, B.S.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 5272-5276, 1991  
 A;Title: A single base insertion in the putative transmembrane domain of the tyrosinase  
 A;Reference number: A40597; MUID:91271371; PMID:1711223  
 A;Accession: A40597  
 A;Molecule type: mRNA

A;Residues: 1-165, 'I', 167-489, 'CPAGRACELAVSSQEKAAS' &lt;CHI&gt;

A;Cross-references: GB:MT4314

A;Experimental source: albinobalbo melanocytes

A;Note: mutant protein is isolated from patient with tyrosinase-negative oculocutaneous albinism

R.Kwon, B.-S.; Haq, A.K.; Pomerantz, S.H.; Halaban, R.

Proc. Natl. Acad. Sci. U.S.A. 84, 7473-7477, 1987

A;Title: Isolation and sequence of a cDNA clone for human tyrosinase that maps at the mct locus

A;Reference number: A94185; MUID:88041128; PMID:2823263

A;Accession: S04760

A;Molecule type: mRNA

A;Residues: 'L', 2-41, 'TGV', 46-191, 'Y', 193-307, 'T', 309-372, 'HVPGT', 379-401, 'Q', 403-494, 'E'

A;Cross-references: GB:J03581; NID:940027; PIDN:AAA61241.1; PMID:9340028

A;Experimental source: normal melanocytes

A;Note: the sequence differs from that shown in several regions due to reading frameshift

R.Wittbier, A.; Odh, G.; Rosengren, E.M.; Rorman, H.

Acta Derm. Venereol. 70, 291-294, 1990

A;Title: Isolation of soluble tyrosinase from human melanoma cells.

A;Reference number: A60149; MUID:91021767; PMID:1977251

A;Accession: A60149

A;Molecule type: protein

A;Residues: 19-23, 'X', 25-28 &lt;WIT&gt;

A;Note: the sequence was determined from a soluble form of the enzyme from melanoma cell

A;Accession: B60149

A;Molecule type: protein

A;Residues: 1-22, 'X', 25-34, 'XX', 37-38 &lt;WIT2&gt;

A;Note: the sequence was determined from a membrane-bound form of the enzyme from melanoma cells

R.Giebel, L.B.; Strunk, K.M.; Spritz, R.A.

submitted to the EMBL Data Library, July 1991

A;Description: Organization and nucleotide sequences of the human tyrosinase gene and a

A;Reference number: S53560

A;Accession: S53560

A;Molecule type: protein

A;Cross-references: EMBL:ME63238

R.Wittbier, A.; Dahlbaeck, B.; Odh, G.; Rosengren, A.M.; Roszman, H.

Acta Derm. Venereol. 69, 125-131, 1989

A;Title: Isolation of human tyrosinase from cultured melanoma cells.

A;Reference number: A60464; MUID:89163645; PMID:2564229

A;Accession: A60464

A;Molecule type: protein

A;Residues: 'L', 2-11; 19-23, 'X', 25-34, 'XX', 37-38 &lt;WIT2&gt;

R.Guo, Z.; Guiffoye, R.A.; Thiel, A.J.; Wang, R.; Smith, L.M.

Nucleic Acids Res. 22, 5456-5465, 1994

A;Title: Direct fluorescence analysis of genetic polymorphisms by hybridization with oligonucleotides: application of a tyrosinase gene of GM116340.

A;Reference number: S53559; MUID:95116340; PMID:816638

A;Content: annotation

C;Comment: This cell-specific oxidase is a glycoprotein containing two Cu per enzyme; it

C;Reactions: reactions in the formation of pigments such as melanins and other polyphenolic compound

C;Genetics:

A;Gene: GDB:TYR

A;Cross-references: GDB:120476; OMIM:203100

A;Map position: 11q21-11q21

A;Introns: 273/3; 346/1; 395/2; 455/1

C;Superfamily: monophenol monooxygenase

C;Keywords: albinism; copper; glycoprotein; melanin biosynthesis; monooxygenase; oxidoreductase

F;1-18/Domain: signal sequence #status predicted &lt;SIG&gt;

F;19-529/Domain: monophenol monooxygenase #status experimental &lt;MAT&gt;

F;47-500/Domain: transmembrane carbohydrate site: carbohydrate (An) (covalent) #status predicted

F;86,111,161,210,337,371/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;363,367,390,420/Binding site: copper (His) #status predicted

F;363,367,390,420/Binding site: copper (His) #status predicted

Query Match Score: 100.0%; Score: 83; DB: 1; Length: 529;

Best Local Similarity: 100.0%; Pred. NO.: 1.3e+00; Matches: 15; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Qy 1 DYSYQLQDSDPNSFQD 15

Db 448 DYSYQLQDSDPNSFQD 462

monophenol monooxygenase (EC 1.14.18.1) precursor [validated] - mouse

N;Alternate names: cresolase; monophenol oxidase; phenolase;

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1989 #sequence revision 31-Mar-1989 #text change 20-Apr-2000

C;Accession: A27711; A60778; A32429; B32429; S01170; S02778; S15753; I49736

R.Kwon, B.S.; Wakulchik, M.; Haq, A.K.; Halaban, R.; Kestler, D.

Biochem. Biophys. Res. Commun. 153, 1301-1309, 1988

A;Title: Sequence analysis of mouse tyrosinase cDNA and the effect of melanotropin on its

A;Reference number: A27711; MUID:88268910; PMID:3134020

A;Accession: A27711

A;Molecule type: mRNA

A;Residues: 1-533 &lt;KRN&gt;

A;Cross-references: GB:ME0234; NID:9202247; PIDN:AAA40516.1; PMID:9202248

A;Experimental source: Cloudman S-91 melanoma cells

R.Kwon, B.S.; Haq, A.K.; Wakulchik, M.; Kestler, D.; Barton, D.R.; Francke, U.; Lamoreux

J. Invest. Dermatol. 93, 589-594, 1989

A;Title: Isolation, chromosomal mapping, and expression of the mouse tyrosinase gene.

A;Reference number: A60778; MUID:90010220; PMID:2507645

A;Accession: A60778

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-273 &lt;KN22&gt;

A;Cross-references: BALB/c

A;Experimental source: Tabe, I.; Garattini, E.; Sartori, D.; Studer, M.; Mintz, B.

R.Terao, M.; Tabe, I.; Garattini, E.; Sartori, D.; Studer, M.; Mintz, B.

Biochem. Biophys. Res. Commun. 159, 848-853, 1989

A;Title: Isolation and characterization of variant cDNAs encoding mouse tyrosinase.

A;Reference number: A32429; MUID:89193679; PMID:2494997

A;Accession: A32429

A;Molecule type: mRNA

A;Residues: 1-102, 'C', 104-345, 'G', 347-533 &lt;TER&gt;

A;Cross-references: GB:ME24560; NID:9202249; PIDN:AAA40517.1; PMID:9202250

A;Experimental source: B32429

A;Molecule type: DNA

A;Residues: 1-77-155-345, 'G', 347-533 &lt;TE2&gt;

A;Cross-references: GB:ME24560

A;Experimental source: B16 melanoma cells

R.Mueller, G.; Ruppert, S.; Schmid, E.; Schuetz, G.

EMBO J. 7, 2733-2730, 1988

A;Title: Functional analysis of alternatively spliced tyrosinase gene transcripts.

A;Reference number: S01170; MUID:89090636; PMID:3141148

A;Accession: S01170

A;Molecule type: mRNA

A;Residues: 1-102, 'C', 104-263, 'I', 265-345, 'G', 347-533 &lt;MCB&gt;

A;Cross-references: GB:XI2782; NID:95061; PIDN:CAA1273.1; PMID:955062

R.Yamamoto, H.; Takeuchi, S.; Kido, T.; Makino, K.; Nakata, A.; Shinoda, T.; Takeuchi, T.

Jpn. J. Genet. 62, 271-274, 1987

A;Title: Cloning and sequencing of mouse tyrosinase cDNA.

A;Reference number: S02278

A;Accession: S02278

A;Molecule type: mRNA

A;Residues: 1-102, 'C', 104-263, 'I', 265-345, 'G', 347-448 &lt;YAM&gt;

A;Cross-references: EMBL:X12782

A;Title: Part of this sequence was confirmed by protein sequencing

R.Shibahara, S.; Okina, Y.; Takeda, A.; Yamamoto, H.; Takeuchi, C.

Eur. J. Biochem. 189, 455-461, 1990

A;Title: A point mutation in the tyrosinase gene of BALB/c albino mouse causing the cysteine residue substitution.

A;Reference number: S515753; MUID:9029939; PMID:2110899

A;Accession: S15753

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-13 &lt;SH1&gt;

A;Cross-references: EMBL:X51743; NID:955057; PIDN:CAA36033.1; PMID:955058

A;Experimental source: strain BALB/c

R.Kwon, B.S.; Halaban, R.; Chintamani, C.

Biochem. Biophys. Res. Commun. 161, 252-260, 1989

A;Title: Molecular basis of mouse Himalayan mutation.

A;Reference number: I49736; MUID:89223644; PMID:2567165

A;Accession: I49736

A;Status: preliminary; translated from GB/EMBL/DDBu

A;Molecule type: mRNA

A;Residues: 1-39, 'I', 41-102, 'C', 104-196, 'Q', 198-345, 'G', 347-419, 'R', 421-533 &lt;RES&gt;

A;Cross-references: GB:ME2729; NID:9193845; PIDN:AAA37006.1; PMID:9309396

C;Comment: This cell-specific oxidase is a glycoprotein containing two Cu per enzyme; it

RESULTS 2

YRMSCS

reactions in the formation of pigments such as melanins and other polyphenolic compound  
 ;Gene: Tyr1  
 ;Map position: 7  
 ;Superfamily: monophenol monooxygenase  
 ;Keywords: albinism; alternative splicing; copper; glycoprotein; melanin biosynthesis;  
 ;  
 F11-18;Domain: signal sequence #status Predicted <SG>  
 F11-19-533;Product: monophenol monooxygenase #status Predicted <MAT>  
 F11-474-497;Domain: transmembrane #status Predicted <TMM>  
 F11-86,111-161,230,337,371;Binding site: carbohydrate (Asn) (covalent) #status predicted

Query	Match	Score	DB	Length			
Q2Y	1 DYSYIQLQSPDPDSFD 15  :   :   :   : 448 DYSYIQLQESPPGFYRN 462	55.1%	54;	1;			
D2b		Best Local Similarity	60.0%;	Pred. No.	0.66;		
	Matches	9;	Conservative	4;	Mismatches	2;	
				Indels	0;	Gaps	0;

**RESULT 3**

Ag9416  
 L-3-hydroxy-2-methylpropanoyl-β-D-pyruvate formate-lyase activating enzyme (act-3) homolog - *Archaeoglobus fulgidus*  
 L-Accession: A69416  
 L-Accession: A69416  
 L-Cl: Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.C.; Gill, S.; Kirkeness, E.P.; Gldeker, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
 L-Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon *Archaeoglobus fulgidus*.  
 L-Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artich, P.; Kaine, B.P.; Sykes, S.; Smith, H.O.; Woese, C.R.; Venter, J.C.  
 L-Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon *Archaeoglobus fulgidus*.  
 L-Reference number: A69416  
 L-Accession: A69416  
 L-Accession: A69416  
 L-Accession: A69416  
 L-Molecule type: DNA  
 L-Residues: 1-336 <KLE>  
 L-Cross references: GB:AB0001012; GB:AB000782; NID:92689335; PID:AA89917.1; PID:9264924  
 L-Superfamily: conserved hypothetical protein MJ0808

Query	Match	Score	DB	Length			
Q2Y	1 DYSYIQLQSPDPDS 12  :   :   :   : 100 DYSYIQLREIDDDT 111	59.0%	49;	1;			
D2b		Best Local Similarity	66.7%;	Pred. No.	2.5;		
	Matches	8;	Conservative	3;	Mismatches	1;	
				Indels	0;	Gaps	0;

**RESULT 4**

JW0077  
 chitinase (EC 3.2.1.14) α - Gladiolus gandavensis  
 C-Species: Gladiolus gandavensis  
 C-Accession: JW0077  
 C-Accession: JW0077  
 C-Biosci: Biotechnol. Biochem. 62, 38-389, 1998  
 C-Author: Complete amino acid sequence of chitinase-a from bulbs of gladiolus (Gladiolus gandavensis). Reference number: JW0077; PMID:9532802  
 C-Molecule type: protein  
 C-Accession: JW0077  
 C-Residues: 1-1274 <YAM>  
 C-Comment: This enzyme hydrolyzes beta-1,4-linked N-acetylglucosamine polymer chitin.  
 C-Superfamily: alcohol sulfotransferase  
 C-Keywords: glycosidase; hydrolase

Query	Match	Score	DB	Length			
Q2Y	1 DYSYIQLQSPDPDS 12  :   :   :   : 100 DYSYIQLREIDDDT 111	54.2%	45;	2;			
D2b		Best Local Similarity	66.7%;	Pred. No.	9;		
	Matches	7;	Conservative	4;	Mismatches	4;	
				Indels	0;	Gaps	0;

RESULT 5	
AC1142	N-acyl-L-amino acid amidohydrolase
C;Species:	Listeria monocytogenes
C;Date:	27-Nov-2001 #sequence_rev
C;Accession:	AC1142
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Dominguez-Bernal, G.; Duchaud, D.; Jones, L.M.; Karst, U.	
A;Authors:	Kreft, J.; Kuhn, M.; Kuehne, C.; Schlueter, T.; Simoes, N.
A;Title:	Comparative Genomics of
A;Reference number:	AB1077; MUID:
A;Accession:	AC1142
A;Status:	preliminary
A;Molecule type:	DNA
A;Residues:	1-393 <GLA>
A;Cross-references:	GB:NC_003210;
A;Experimental source:	strain EGD
C;Genetics:	
A;Gene:	lm0538
C;Superfamily:	hippurate hydrolases
Query Match	54.2%
Best Local Similarity	61.5%
Matches	8 ; Conservative
Qy	1 DYSYIQLQSDPDSF 13
Db	333 DFSYFQDEAPGSF 345

  

RESULT 6	
AF1500	N-acyl-L-amino acid amidohydrolase
C;Species:	Listeria innocua
C;Date:	27-Nov-2001 #sequence_rev
C;Accession:	AF1500
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Dominguez-Bernal, G.; Duchaud, D.; Jones, L.M.; Karst, U.	
A;Authors:	Kreft, J.; Kuhn, M.; Kuehne, C.; Schlueter, T.; Simoes, N.
A;Title:	Comparative Genomics of
A;Reference number:	AB1077; MUID:
A;Accession:	AF1500
A;Status:	preliminary
A;Molecule type:	DNA
A;Residues:	1-393 <GLA>
A;Cross-references:	GB:AL592022;
A;Experimental source:	strain C11
C;Genetics:	
A;Gene:	lin0542
C;Superfamily:	hippurate hydrolases
Query Match	54.2%
Best Local Similarity	61.5%
Matches	8 ; Conservative
Qy	1 DYSYIQLQSDPDSF 13
Db	333 DFSYFQDEAPGSF 345

  

RESULT 7	
CB4687	acyl-L-fatty acid elongase [imm
C;Species:	
C;Date:	
C;Accession:	
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Dominguez-Bernal, G.; Duchaud, D.; Jones, L.M.; Karst, U.	
A;Authors:	Kreft, J.; Kuhn, M.; Kuehne, C.; Schlueter, T.; Simoes, N.
A;Title:	Comparative Genomics of
A;Reference number:	AB1077; MUID:
A;Accession:	CB4687
A;Status:	preliminary
A;Molecule type:	DNA
A;Residues:	1-393 <GLA>
A;Cross-references:	GB:AL592022;
A;Experimental source:	strain C11
C;Genetics:	
A;Gene:	lin0542
C;Superfamily:	acyl-L-fatty acid elongase [imm
Query Match	54.2%
Best Local Similarity	61.5%
Matches	8 ; Conservative
Qy	1 DYSYIQLQSDPDSF 13
Db	333 DFSYFQDEAPGSF 345

C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 25-Aug-2003  
C;Accession: CB1687  
R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;  
Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the Plant Arabidopsis thaliana.  
A;Reference number: A84420; PMID:20083487; PMID:10617197  
A;Accession: CB1687  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-476 <STO>  
A;Cross-references: GB:AE002093; NID:94580394; PIDN:AAD24372-1; GSPDB:GN00139  
C;Genetics:  
A;Gene: AtCG28630  
A;Map position: 2  
C;Superfamily: very-long-chain 3-ketoacyl-CoA synthase  
Query Match Score 45; DB 2; Length 476;  
Best Local Similarity 46.2%; Pred. No. 17;  
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
QY 2 YSYLQDSDPDSFQ 14  
Db 458 FGNIQDDEDPDTFK 470

RESULT 8  
T38629 hypothetical protein SPAC31G5.12c - fission yeast (Schizosaccharomyces pombe)  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C;Accession: T38629  
R;McLean, J.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.  
submitted to the EMBL Data Library, September 1997  
A;Reference number: Z21122  
A;Accession: T38629  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: DNA  
A;Residues: 1-150 <MCML>  
A;Cross-references: EMBL:Z98979; PIDN:CAB11696-1; GSPDB:GN00066; SPDB:SPAC31G5.12C  
A;Experimental source: strain 972h-; cosmid c31G5  
C;Genetics:  
A;Gene: SPDB:SPAC31G5.12C  
A;Map position: 1

Query Match Score 43; DB 2; Length 150;  
Best Local Similarity 57.1%; Pred. No. 9.6;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
QY 2 YSYLQDSDPDSFQ 15  
Db 70 YSYTPDSDPYGD 83

RESULT 9  
S56790 probable membrane protein YJL019w - yeast (Saccharomyces cerevisiae)  
N;Alternate names: hypothetical protein J1310  
C;Species: Saccharomyces cerevisiae  
C;Date: 08-Jul-1995 #sequence\_revision 08-Sep-1995 #text\_change 19-Apr-2002  
C;Accession: S56790  
R;To Van, D.; Perea, J.; Jacq, C.  
submitted to the Protein Sequence Database, September 1995  
A;Reference number: S56790  
A;Accession: S56790  
A;Molecule type: DNA  
A;Residues: 1-620 <DEH>  
A;Cross-references: EMBL:Z49294; NID:91006737; PIDN:91006738; GSPDB:GN00010; MIPS:YJL019  
C;Genetics:  
A;Gene: MIPS:YJL019w  
A;Cross-references: SGD:S0003556

A;Map position: 10L  
C;Superfamily: Saccharomyces cerevisiae probable membrane protein YJL019w  
C;Keywords: transmembrane protein  
Query Match Score 43; DB 2; Length 620;  
Best Local Similarity 53.8%; Pred. No. 48;  
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DYSYLNQDSDPDSF 13  
Db 116 DKSFTEDSDPSDY 128

RESULT 10  
HB4126 cation efflux system BH3816 [imported] - Bacillus halodurans (strain C-125)  
C;Species: Bacillus halodurans  
C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
C;Accession: HB4126  
R;Takami, H.; Nakasono, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai  
Nucleic Acids Res. 28, 4317-4331, 2000  
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A;Reference number: A83350; MUID:20512582; PMID:11058132  
B;Accession: HB4126  
B;Status: preliminary  
B;Molecule type: DNA  
B;Residues: 1-1093 <STO>  
B;Cross-references: GB:AP001520; GB:BA000004; NID:910176401; PIDN:BA007535-1; GSPDB:GN000  
B;Experimental source: strain C-125  
C;Genetics:  
A;Gene: BH3816

Query Match Score 43; DB 2; Length 1093;  
Best Local Similarity 58.3%; Pred. No. 91;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 4 YLQDSDPDSFQD 15  
Db 662 YLSDSDPDRLE 673

RESULT 11  
JH0720 canabin - African clawed frog  
C;Species: Xenopus laevis (African clawed frog)  
C;Accession: JH0720  
R;Hermann-Brivaniol, A.; Mann, R.W.; Harland, R.M.  
Neuron 9, 417-428, 1992  
A;Title: A protein expressed in the growth cones of embryonic vertebrate neurons defines  
A;Reference number: JH0720; MUID:92398961; PMID:1524825  
A;Accession: JH0720  
A;Molecule type: mRNA  
A;Residues: 1-1744 <HEM>  
A;Cross-references: GB:M99387; NID:9214816; PIDN:AAA49966-1; PMID:9214817  
A;Experimental source: tadpole head  
C;Keywords: intermediate filament

Query Match Score 43; DB 2; Length 1744;  
Best Local Similarity 53.3%; Pred. No. 1.5e-02;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLNQDSDPDSFQD 15  
Db 941 EVDYLQNYDSDPSFQN 955

RESULT 12  
S57964 lipoxygenase (EC 1.11.11.12) - common tobacco  
C;Species: Nicotiana tabacum (common tobacco)  
C;Genetics:  
A;Gene: MIPS:YJL199  
A;Cross-references: SGD:S0003556

Ri'Veronesi, C.; Fournier, J.; Rickauer, M.; Esquerre-Tugaye, M.T.  
submitted to the EMBL Data Library, January 1995  
A;Description: Nucleotide sequence of an elicitor-induced tobacco lipoxygenase cDNA.  
A;Reference number: S57964  
A;Accession: 557964  
A;Status: Preliminary  
A;Molecule type: mRNA  
A;Residues: 1-862 <VER>  
A;Cross-references: EMBL:X84040; PID:9899343; PMID:9899344  
C;Superfamily: lipoxygenase  
C;Keywords: oxidoreductase

Query Match 51.2%; Score 42.5%; DB 2; Length 862;  
Best Local Similarity 56.2%; Pred. No. 84;  
Matches 9; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Qy 1 DSYLQD-SPPDSFQD 15  
Db 200 DYAYNDLGPDKGQD 215

RESULT 13

F71417 cytochrome P450 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
A;Variety: Columbia  
C;Date: 03-Aug-1998 #sequence\_revision 03-Aug-1998 #text\_change 20-Jun-2000  
C;Accession: F71417  
R;Bevan, M.; Bancroft, I.; Bent, B.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk P.; Wedler, H.; Wedler, B.; Wambutt, R.; Weitzneger, T.; Poal, T.M.; Terry, N.; Giel avanagh, T.; Tempel, S.; Koetter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.  
Nature 391, 485-488, 1998  
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Puidomenech C.; Chalwatzi, N.; Jones, J.D.G.; Enyea, T.; Palme, K.; Benes, V.; Rechman, S.; Anserio, A.; Moores, T.; Goldberg, E.B.  
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal  
A;Reference number: A71400; MUID:98121113; PMID:9461215  
A;Accession: F71417  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-184 <BEV>  
A;Cross-references: GB:Z97339; PID:92244891

A;Map Position: 4COP9-4G3.845  
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology F:308-474; domain: cytochrome P450 homology <P45>  
F:452/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 49.4%; Score 41; DB 2; Length 517;  
Best Local Similarity 61.5%; Pred. No. 82; Mismatches 4; Indels 0; Gaps 0;

Qy 3 SYLQDSDPSFQD 15  
Db 404 SYAMMRDPDSWQD 416

RESULT 14

D70034 oligo-1,6-glucosidase homolog yvdL - Bacillus subtilis  
C;Species: Bacillus subtilis  
C;Accession: D70034  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Jun-2000  
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berger C.; Bron, S.; Brönnillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997  
A;Authors: Fouger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galloie, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullio, M.F.; Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurida, K.; Lardinois, A.; Lardinois, Y.; M.; Ogawa, K.; Ogiwara, A.; Onega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Result No.	Score	Query	Match Length	DB ID	Description
1	83	BLOSUM62	100.0	Gapext 0.5	P14679 homo sapien
2	54	Gapop 10.0 , Gapext 0.5	65.1	141681 seqs, 52070155 residues	P11344 mus musculus
3	45	Total number of hits satisfying chosen parameters:	54.2		P19816 <i>Salmonella</i> P55024 <i>Salinus gall</i>
4	45	Minimum DB seq length: 0	54.2		Q9ncp1 <i>Giardia lam</i>
5	43	Maximum DB seq length: 2000000000	51.8		Q9rdy2 <i>legionella</i> P47069 <i>saccharomyces</i>
6	43	Post-processing: Minimum Match 0%	51.8		Q01550 <i>xenopus lae</i>
7	43	Maximum Match 100%	62.0		Q06994 <i>bacillus su</i>
8	43	Listing First 45 summaries	51.8		Q95863 <i>homo sapien</i>
9	41	Database : SwissProt_42:*	49.4		P13331 <i>bacterioph</i>
10	40		48.8		P19217 <i>bos taurus</i>
11	40		48.2		P20910 <i>streptomyce</i>
12	40		48.2		Q05235 <i>mycobacteri</i>
13	40		48.2		P17405 <i>homo sapien</i>
14	40		48.2		P11439 <i>pseudomonas</i>
15	40		48.2		Q8csfh5 <i>staphylococ</i>
16	40		48.2		Q92gz7 <i>richettsia</i>
17	39		47.0		Q58121 <i>methanococc</i>
18	39		47.0		P54645 <i>rattus norv</i>
19	39		47.0		Q13131 <i>homo sapien</i>
20	39		47.0		P10916 <i>caenorhabdi</i>
21	39		47.0		Q9bgd8 <i>halobacteri</i>
22	39		47.0		Q9zpv5 <i>arabidopsis</i>
23	39		47.0		Q09229 <i>caenorhabdi</i>
24	39		47.0		Q9bwj3 <i>mus musculus</i>
25	39		47.0		P22523 <i>escherichia</i>
26	39		47.0		Q9fgz4 <i>arabidopsis</i>
27	39		47.0		Q9rl1 <i>corynebacte</i>
28	38		46.4		Q9vv65 <i>drosophila</i>
29	38		47.0		P37137 <i>xenopus lae</i>
30	38		45.8		Q8tk94 <i>methanosc</i>
31	38		45.8		Q9pmus campylobact
32	38		45.8		P37137 <i>xenopus lae</i>
33	38		45.8		PRTG_ERWCH

- RL J. Exp. Med. 178:489-495(1993).  
 RN [7] SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT TYR-192.  
 RP MEDLINE=21026558; PubMed=1115399;  
 RX MARTINEZ-ARIAS R., COMAS D., ANDRES A., ABELLO M.T., DOMINGO-ROURA X.,  
 RA BERTRAPETIT J., "The tyrosinase gene in gorillas and the albinism of 'Snowflake'.";  
 RA PIGMENT CELL RES. 13:467-470(2000).  
 RL [8] SEQUENCE FROM N.A. (ISOFORM 2).  
 RP TISSUE-SKIN; PubMed=12477932;  
 RX MEDLINE=22388257; PubMed=90241133;  
 RA STRAUSBERG R.L., FEINGOLD E.A., GROUSE L.H., DERGE J.G.,  
 RA SHENMEN C.M., SCHULER G.D.,  
 RA ALTSCHUL S.F., ZEEBERG B., BUTOW K.H., SCHAEFER C.F., BHAT N.K.,  
 RA HOPKINS R.F., JORDAN H., MOORE T., WANG J., HSIEH F.,  
 RA STAPLETON M., SOARES M.B., BONALDO M.F., CASAVANT T.L., SCHEETZ T.B.,  
 RA BROWNSTEIN M.J., USDIN T.B., TOSHIYUKI S., CARNINCI P., PRANGE C.,  
 RA RAHA S.S., LOQUELLANO N.A., PETERS G.J., CARNINCI P., MULLAHY S.J.,  
 RA BOZAK S.A., McEWAN P.J., MCKERNAN K.J., MALEK J.A., GUNARATE P.R.,  
 RA RICHARDS S., WORLEY K.C., HALE S., GARCIA A.M., GAY L.J., HULYK S.W.,  
 RA VILLALON D.K., MUZNY D.M., SODERGREN E.J., LU X., GIBBS R.A.,  
 RA FAHEY J., HEITON B., KETTEMAN M., MADAN A., RODRIGUES S., SANCHEZ A.,  
 RA WHITING M., MADAN A., YOUNG A.C., SHEVCHENKO Y., BONIFFARD G.G.,  
 RA BLAKESLEY R.W., TOUCHMAN J.W., GREEN E.D., DICKSON M.C.,  
 RA RODRIGUZ A.C., GRIMWOOD J., SCHMITZ J., MYERS R.M.,  
 RA BUTTERFIELD Y.S.N., KRZYWIANSKI M.I., SKALSKA U., SMAILUS D.E.,  
 RA SCHNERRICH A., SCHEIN J.B., JONES S.J.M., MARRA M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences";  
 RL PROC. NATL. ACAD. SCI. U.S.A. 99:16899-16903 (2002).  
 RN [9] SEQUENCE OF 1-272 FROM N.A.  
 RP TISSUE-LIVER; PubMed=90059403; PubMed=2480811;  
 RX MEDLINE=89351001; PubMed=2504160;  
 RA KIKUCHI H., MIURA H., YAMANOTO H., TAKEUCHI T., DEI T., WATTANABE M.;  
 RT "Characteristic sequences in the upstream region of the human  
 tyrosinase gene.",  
 RT PRECURSOR.;  
 RL BIOCHIM. BIOPHYS. ACTA 1009:283-286 (1989).  
 RN [10] SEQUENCE OF 1-32 FROM N.A.  
 RP TISSUE-LIVER; PubMed=211082082; PubMed=11214319;  
 RX MEDLINE=92048465; PubMed=1943886;  
 RA TAKEDA A., TOMITA Y., OKINAGA S., TAGAMI H., SHIBAHARA S.;  
 RT "Functional analysis of the cDNA encoding human tyrosinase  
 precursor.";  
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 162:984-990 (1989).  
 RN [11] SEQUENCE OF 54-195 FROM N.A., AND VARIANT TYR-192.  
 RP MEDLINE=91404054; PubMed=10094567;  
 RX OERTLING W.S., KING R.A.;  
 RA MURPHY W.J., EIZIRIK E., JOHNSON W.E., ZHANG Y.P., RYDER O.A.,  
 RA O'BRIEN S.J.;  
 RT "Molecular phylogenetics and the origins of placental mammals.";  
 RL NATURE 409:614-618 (2001).  
 RN [12] REVIEW ON OCA VARIANTS.  
 RP MEDLINE=93237884; PubMed=8477259;  
 RA OERTLING W.S., KING R.A.;  
 RT "Molecular basis of type I (tyrosinase-related) oculocutaneous  
 albinism: mutations and polymorphisms of the human tyrosinase gene.";  
 RT "Molecular analysis of type I-A (tyrosinase negative) oculocutaneous  
 albinism.";  
 RL HUM. MUTAT. 2:1-6 (1993).  
 RN [13] REVIEW ON OCA-I VARIANTS.  
 RP MEDLINE=91404054; PubMed=10094567;  
 RX OERTLING W.S., KING R.A.;  
 RA "Molecular basis of albinism: mutations and polymorphisms of  
 pigment genes associated with albinism.";  
 RT "Mutations of the tyrosinase gene in Indo-Pakistani patients with type  
 I (tyrosinase-deficient) oculocutaneous albinism (OCA)." ;  
 RL HUM. MUTAT. 13:99-115 (1999).  
 RN [14] VARIANTS TYR-192; GLN-328; ARG-419 AND LEU-431.  
 RP MEDLINE=94070865; PubMed=1902671;  
 RX TRIPATHI R.K., BUNDEY S., MUSARELLA M.A., DROETTO S., STRUNK K.M.,  
 RA HOLMES S.A., SPRITZ R.A.;  
 RT "Mutations of the tyrosinase gene in Indo-Pakistani patients with type  
 I (tyrosinase-deficient) oculocutaneous albinism (OCA)." ;  
 RL HUM. MUTAT. 53:1173-1179 (1993).  
 RN [15] VARIANTS OCA-IA SER-217 DEL; HIS-299 AND LYS-373, AND VARIANTS  
 RX MEDLINE=90259036; PubMed=2342539;  
 RA SPRITZ R.A., STRUNK K.M., GIEBEL L.B., KING R.A.;  
 RT "Detection of mutations in the tyrosinase gene in a patient with type  
 OCA-IB SER-152 AND LYS-294.";  
 RP MEDLINE=94175072; PubMed=128955;

Query Match Similarity 100.0%; Score 83; DB 1; Length 529;  
 Best Local Similarity 100.0%; Prod. No. 1.le-05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYIQLQDSDPDSFQD 15  
 Db 448 DYSYIQLQDSDPDSFQD 462

RESULT 2

TYRO\_MOUSE STANDARD; PRT; 533 AA.

ID TYRO\_MOUSE STANDARD; PRT; 533 AA.

AC P11344; DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 08-FEB-2003 (Rel. 41, Last annotation update)

DE Tyrosinase Precursor (EC 1.14.18.1) (Monophenol monooxygenase)  
 DE (Albino locus protein).

GN TYR.

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId:10090;

RN [1]

RP SEQUENCE FROM N.A.  
 STRAIN=DB/1/2J;

RX MEDLINE=82268910; PubMed=3134020;  
 RA Kwon B.S.; Wakulchik M.; Haq A.K.; Halaban R.; Kestler D.;  
 RT "Sequence analysis of mouse tyrosinase cDNA and the effect of  
 melanotropin on its gene expression."  
 RL Biochem. Biophys. Res. Commun. 153:1301-1309(1988).

RN [2]

RP SEQUENCE FROM N.A.  
 STRAIN=Himalayan;

RX MEDLINE=82273644; PubMed=2567165;  
 RA Kwon B.S.; Halaban R.; Chintanamneni C.;  
 RT "Molecular basis of mouse tyrosinase mutation";  
 RL Biochem. Biophys. Res. Commun. 161:252-260(1989).

RN [3]

RP SEQUENCE FROM N.A.  
 MEDLINE=8030636; PubMed=3141148;  
 RA Mueller G.; Ruppert S.; Schmid E.; Schuetz G.;  
 RT "Functional analysis of alternatively spliced tyrosinase gene  
 transcripts";  
 RT EMBO J. 7:2723-2730(1988).

RN [4]

RP SEQUENCE FROM N.A.  
 MEDLINE=8913679; PubMed=2494997;

RX SEQUENCE FROM N.A.  
 MEDLINE=8913679; PubMed=2494997;  
 RA Terao M.; Tabe I.; Garattini E.; Sartori D.; Studdert M.; Mintz B.;  
 RT "Isolation and characterisation of variant cDNAs encoding mouse  
 tyrosinase";  
 RA Yamamoto H.; Takeuchi S.; Kudo T.; Makino K.; Nakata A.; Shinoda T.,  
 RT Takeuchi T.;  
 RT "Cloning and sequencing of mouse tyrosinase cDNA.";  
 RL Jpn. J. Genet. 62:271-274(1987).

RN [6]

RP SEQUENCE OF 1-273 FROM N.A.  
 RX MEDLINE=90212084; PubMed=2517217;

RA Yamamoto H.; Takeuchi S.; Kudo T.; Sato C.; Takeuchi T.;  
 RT "Melanin production in cultured albino melanocytes transfected with  
 mouse tyrosinase cDNA.";  
 RL Jpn. J. Genet. 64:121-135(1989).

RN [7]

RP VARIANT ALBINO.  
 STRAIN=BALB/C;  
 RX MEDLINE=9024393; PubMed=2110899;  
 RA Shibahara S.; Okinaga S.; Tomita Y.; Takeda A.; Yamamoto H.; Sato M.,  
 RA Takeuchi T.

"A point mutation in the tyrosinase gene of BALB/c albino mouse causing the cysteine-->serine substitution at position 85.";  
 VARIANT CHINCHILLA MOUSE.  
 MEDLINE=90360993; PubMed=2118105;  
 RA Beermann F.; Ruppert S.; Hummler E.; Bosch F.X.; Mueller G.,  
 RA Rusther U.; Schuetz G.;  
 RT "Rescue of the albino phenotype by introduction of a functional tyrosinase gene into mice.";  
 RT EMBO J. 9:2819-2826(1990).

-!- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC COMPOUNDS. CATALYZES THE RATE-LIMITING CONVERSIONS OF TYROSINE TO DOPA, DOPA TO DOPA-QUINONE AND POSSIBLY 5,6-DIHYDROXYINDOLE TO INDOLE-5,6 QUINONE.

CC -!- CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O (2) = L-DOPA + DOPAquinone + H (2)O.

CC -!- COFACTOR: Binds 2 copper ions per subunit.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Melanosomal.

CC -!- DISEASE: DEFECTS IN TYR RESULT IN VARIOUS FORMS OF ALBINISM. HIMALAYAN STRAIN TYROSINASE IS TEMPERATURE-SENSITIVE.

CC -!- SIMILARITY: Belongs to the tyrosinase family.

CC -!- CAUTION: REF 4 SEQUENCE WAS INCORRECT DUE TO A DELETION OF EXON 3.

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CC DR EMBL; D00440; BAA0341.1;  
 DR EMBL; M20234; AAA00516.1;  
 DR EMBL; M26729; AAA37806.1;  
 DR EMBL; X12782; CAA31273.1;  
 DR EMBL; M24560; AAA00517.1;  
 DR EMBL; D00131; BAA00079.1;  
 DR EMBL; X51743; CAA36033.1;  
 DR EMBL; D00439; BAA00340.1;  
 DR PIR; A22771; YRMSCS.  
 DR MGD; MGI:38880; TYR.  
 DR InterPro; IPR008922; Di-cooper\_centre.  
 DR InterPro; IPR002227; Tyrosinase.  
 DR PRINTS; PR00032; TYROSINASE.  
 DR PROSITE; PS00497; TYROSINASE\_1.1.  
 DR PROSITE; PS00598; TYROSINASE\_2.1.  
 KW Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Signal;  
 KW Transmembrane; Melanin biosynthesis; Disease mutation; Albinism.

CC FT SIGNAL 1 18  
 FT CHAIN 19 533  
 FT DOMAIN 19 476  
 FT TRANSEM 477 497  
 FT DOMAIN 498 533  
 FT METAL 180 180  
 FT METAL 202 202  
 FT METAL 211 211  
 FT METAL 363 363  
 FT METAL 367 367  
 FT METAL 390 390  
 FT DOMAIN 503 508  
 FT CARBOHYD 86 86  
 FT CARBOHYD 111 111  
 FT CARBOHYD 161 161  
 FT CARBOHYD 230 230  
 FT CARBOHYD 337 337  
 FT CARBOHYD 371 371  
 FT CARBOHYD 103 103  
 FT VARIANT 420 420  
 FT VARIANT 482 482  
 FT VARIANT 40 40

CC -!- C (IN ALBINO MICE).  
 CC -!- S (IN HIMALAYAN STRAIN).  
 CC -!- T (IN CHINCHILLA MICE).  
 CC -!- I (IN REF. 2).  
 CC -!- M -> I (IN REF. 40).



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 CC

DR EMBL; D88349; BAA1350.1; -.  
 DR EMBL; L46805; AAB0844.1; -.  
 DR PIR; PC4153; PCA153.  
 DR InterPro; IPR008922; Di\_copper\_centre.  
 DR InterPro; IPR00227; Tyrosinase.  
 DR Pfam; PF0264; tyrosinase\_1.  
 DR PRINTS; PS00498; TYROSINASE\_1; 1.  
 DR PROSITE; PS00092; TYROSINASE\_2; 1.  
 DR OXIDOREDUCTASE; Monooxygenase\_Copper; Glycoprotein; Signal;  
 KW Transmembrane; Melanin biosynthesis.  
 KW SIGNAL\_1  
 FT CHAIN 19 529 TYROSINASE  
 FT DOMAIN 19 476 IUMENAL, MELANOSOME (POTENTIAL).  
 FT TRANSMEM 477 497 POTENTIAL.  
 FT DOMAIN 498 529 CTOPLASMIC (POTENTIAL).  
 FT METAL 180 180 COPPER\_A (BY SIMILARITY).  
 FT METAL 202 202 COPPER\_A (BY SIMILARITY);  
 FT METAL 211 211 COPPER\_A (BY SIMILARITY);  
 FT METAL 363 363 COPPER\_B (BY SIMILARITY);  
 FT METAL 367 367 COPPER\_B (BY SIMILARITY).  
 FT CARBOHYD 390 390 COPPER\_B (BY SIMILARITY).  
 FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 529 AA; 60357 MW; 74B464A5C3EBFB5 CRC64;  
 Query Match Score 45%; DB 1; Length 529;  
 Best Local Similarity 60.0%; Pred. No. 12; Gaps 0;  
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 Qy 1 DSYYLQDSDPPNSFQD 15  
 DB 448 DYELYQDPEALGSFQD 462

RESUL 5  
 ERFL\_GIALA STANDARD; PRT; 457 AA.  
 ID\_ERFL\_GIALA STANDARD;  
 AC Q9NCPI;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Eukaryotic peptide chain release factor subunit 1 (erFL) (Eukaryotic  
 DE release factor 1).  
 GN ERFL.  
 OS Giardia lamblia (Giardia intestinalis). Giarditidae; Giardina.  
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardina.  
 OX NCBI\_TaxID:5741;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20293306; PubMed=10833194;  
 RA Inagaki Y., Doolittle W.F.;  
 RT "Evolution of the eukaryotic translation termination system: origins  
 of release factors." Mol. Biol. Evol. 17: 882-889 (2000).  
 CC -!- FUNCTION: Directs the termination of nascent peptide synthesis  
 CC (translation) in response to the termination codons UAA, UAG and  
 CC UGA (By similarity).  
 CC -!- SUBUNIT: Heterodimer of two subunits, one of which binds GTP.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-!- SIMILARITY: Belongs to the eukaryotic release factor 1 family.  
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 CC

CC DR AF198107; AA774402.1; -.  
 DR EMBL; P46055; 1DT9  
 DR HSSP; P46055; 1DT9  
 DR InterPro; IPR00403; erFL.  
 DR InterPro; IPR005140; erFL\_1.  
 DR InterPro; IPR005142; erFL\_2.  
 DR InterPro; IPR005143; erFL\_3.  
 DR Pfam; PF04463; erFL\_1; 1.  
 DR Pfam; PF03464; erFL\_2; 1.  
 DR Pfam; PF03465; erFL\_3; 1.  
 DR TIGRFAMs; TIGR00108; erFL; 1.  
 KW Protein biosynthesis.  
 SQ SEQUENCE 457 AA; 51029 MW; BE185FFFD1F0C943 CRC64;  
 Query Match Score 43%; DB 1; Length 457;  
 Best Local Similarity 58.3%; Pred. No. 21;  
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 Qy 4 YLQDSDPPNSFQD 15  
 DB 440 EMQESDEDSMDM 451  
 RESULT 6  
 G6P1\_LEGEN ID LEGPN STANDARD; PRT; 497 AA.  
 AC Q9RY2Y; ID LEGPN STANDARD;  
 AC 440 EMQESDEDSMDM 451  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose  
 DE isomerase) (PGI) (Phosphohexose isomerase) (PHI).  
 OS Legionella pneumophila.  
 OS Legionellaceae; Gammaproteobacteria; Legionellales;  
 OC Legionellaceae; Legionales;  
 OX NCBI\_TaxID=446;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RCL / Olde / Serogroup 1;  
 RA Lueneberg B., Zettmann N., Hartmann M., Knirel Y.A., Kooistra O.,  
 RA Zaehringen U., Heilig J., Frosch M.;  
 RT "A 30 kb gene cluster involved in biosynthesis of the virulence  
 RT associated lipopolysaccharide carbohydrate moiety of Legionella  
 RT pneumophila."  
 RT Submitted (UNP-1998) to the EMBL/Genbank/DBJ databases.  
 CC ! CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-  
 CC phosphate.  
 CC -!- PATHWAY: Involved in glycolysis and in gluconeogenesis.  
 CC -!- SUBCELLULAR LOCATION: Cyttoplasmic (By similarity).  
 CC -!- SIMILARITY: Belongs to the GPI family.  
 CC

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 CC

CC EMBL; A0007311; CAB65205.1; -.

DR HSSP; Q9N1E2; 1HDX.

DR HAMAP; MF\_00473; 1.

DR InterPro; IPR001672; G6P\_Isomerase.

DR Pfam; PF00342; PGT; 1.  
 DR PRINTS; PR00652; G6PIISOMERASE.  
 DR PROSITE; PS00765; P-GLUCOSE ISOMERASE 1; 1.  
 DR PROSITE; PS00174; P-GLUCOSE ISOMERASE 2; 1.  
 KW Isomerase; Glucuronogenesis; Glycolysis.  
 FT ACT SITE 381 381 BY SIMILARITY.  
 FT ACT SITE 485 485 BY SIMILARITY.  
 SQ SEQUENCE 497 AA; 56091 MW; BCDAA402771310C CRC64;

Query Match Score 43; DB 1; Length 497;  
 Best Local Similarity 46.7%; Pred. No. 23; 0;  
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DYSYIQLQDSDPDSFQD 15  
 Db 180 NYHF1SDVDFASFND 194

**RESULT 7**  
**YJB9 YEAST** STANDARD; PRT; 620 AA.

AC P47079 ;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DT Hypothetical protein 72.4 kDa protein in PBT130-CCR3 intergenic region.  
 DN YJ019W OR J1310.  
 OS Saccharomyces cerevisiae (Baker's Yeast).  
 OC Saccharomyctetes; Fungi; Ascomycota; Saccharomycteaceae; Saccharomyces.  
 OC Saccharomyctetes; Fungi; Ascomycota; Saccharomycteaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;

RN [1]  
 RP Submitted (SEP-1995) to the BMBL/GenBank/DDBJ databases.

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DR PIR: S55790; SS56790;  
 DR Germonline: 141635; -;  
 DR SGD: S000556; YJL019W.  
 DR GO: GO:0006021; C:integral to membrane; IDA.  
 DR GO: GO:0007103; P:nuclear migration during conjugation with c. . .; IMP.  
 DR GO: GO:0007103; P:bind pole body duplication (sensu Sacccha. . .); IMP.

KW Hypothetical protein; Transmembrane; ATP-binding.  
 FT DOMAIN 88 93 POTENTIAL.  
 FT TRANSMEM 155 175 POTENTIAL.  
 FT NP\_BIND 187 194 ATP (POTENTIAL).  
 FT DOMAIN 391 401 POLY-GLN.

SQ SEQUENCE 620 AA; 18EC1346B9A5C6B CRC64;

Query Match Score 43; DB 1; Length 620;  
 Best Local Similarity 53.8%; Pred. No. 30; 0;  
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DYSYIQLQDSDPDSF 13  
 Db 116 DKSFIEDSDSFSY 128

**RESULT 8**  
**TANA\_XENLA** STANDARD; PRT; 1744 AA.

AC Q01555;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)

RA Denizot F.; Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.

[2]

SEQUENCE FROM N.A.

STRAIN=168;

PIR: SEQUENCE FROM N.A.

DR EMBL; Z94043; CAB08041.1; -.

DR EMBL; Z99021; CAB1561.1; -.

DR HSSP; P21332; IUGK.

DR Subtilist; BG12421; mALL.

DR PIR: D70034; D70034.

DR InterPro; IPG106589; Alp\_amyl\_cat\_sub.

DR InterPro; IPRO06047; Alp\_amyl\_cat.

DR SMART; SM00642; Amyl; 1.

DR PF00128; alpha\_amylase; 1.

DR Hydrolase; Glycosidase; Complete proteome.

DR KW BY SIMILARITY.

DR FT ACT SITE 199 199 BY SIMILARITY.

DR FT ACT SITE 255 255 BY SIMILARITY.

DR FT ACT SITE 331 331 BY SIMILARITY.

DR SEQUENCE 561 AA; 66081 MW; 2B43E9A4AD5A222 CRC64;

CC

Query Match 49.4%; Score 41; DB 1; Length 561;

CC

Best Local Similarity 53.8%; Pred. No. 55; Matches 2; Mismatches 4; Indels 0; Gaps 0;

CC

1 DYSYLOQSDPDF 13

CC

484 DYQLQNDPQVF 496

CC

Db 484 DYQLQNDPQVF 496

CC

RESULT 10

CC

SNAL\_HUMAN STANDARD; PRT; 264 AA.

CC

ID SNAL\_HUMAN O95863; Q9PP13; Q9UBP7; Q9UHH7;

CC

AC DT 09-MAY-2000 (Rel. 39, Created)

CC

DT DT 16-OCT-2001 (Rel. 40, Last sequence update)

CC

DT DT 10-OCT-2003 (Rel. 42, Last annotation update)

CC

DE Zinc finger protein SNAII (Snail protein homolog) (Sna protein).

CC

GN SNAII OR SNAH.

CC

OS Homo sapiens (Human).

CC

OC Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CC

NCBI\_TaxID=9606; [1]

CC

RN RN SEQUENCE FROM N.A.

CC

RP RC TISSUE=Hammary gland;

CC

TRUONG T.K., CHEN S.

CC

RT "Isolation and characterization of SnaH, a human gene homologous to

CC

mouse Sna and Drosophila snail gene.";

CC

RT Submitted (FEBB-1999) to the EMBL/GenBank/DDBJ databases.

CC

[2]

CC

RN RN SEQUENCE FROM N.A.

CC

RP RX MEDLINE=20003744; PubMed=10543399;

CC

RA RA TWIGG S.R., WILKIE A.O.M.;

CC

RT "Characterisation of the human snai (SNAIL) gene and exclusion as a

CC

RT major disease gene in craniosynostosis.";

CC

RT mouse Sna and Drosophila snail gene.";

CC

RT Submitted (FEBB-1999) to the EMBL/GenBank/DDBJ databases.

CC

[3]

CC

RN RN SEQUENCE FROM N.A.

CC

RP RX MEDLINE=20054352; PubMed=1058766;

CC

RA RA PAZNIAKAS W.A., OKAJIMA K., SCHERTER M., WOOD S., JABS E.W., BRIDGENAN A.M., BROWN A.J.,

CC

RT "Genomic organization, expression, and chromosome location of the

CC

RT human SNAIL gene (SNAIL) and a related processed pseudogene

CC

(SNAILP).";

CC

RT Genomics 62:42-49 (1999).

CC

[4]

CC

RN RN SEQUENCE FROM N.A.

CC

RP RX MEDLINE=20003744; PubMed=10543399;

CC

RA RA BEAILEY J., BARTLOW K.F., BATES K.N., ASHURST J., BURTON J., GILBERT J.G.R., BAGULEY C.L., DELOUKAIS P., MATTHIWS G., ALMADA J.P., BABBAGE A.K., BEARE D.M., JONES M., STAVRIDIS G., BIRD C.P., BLAKLEY R., BEARD L.M., BEARE D.M., BEASLEY O.P., BIRD C.P., BLAKLEY R., BEARD L.M., BEARE D.M., BROWN A.J., BUCK D., BURILLI W.D., BULMER A.P., CARDE C., CARTER N.P., CHAPMAN J.C., CLAMP M., CLARK L.N., CLARK S.Y., CLEEE C.M., CLEGG S., COBLEY V.E., COLLIER R.E., CONNOR R.E., CORBY N.R., COULLISON A., COVILLE G.J., DEADMAN R., DHAMI P.D., DUNN M., ELLINGTON A.G., FRANKLAND J.A., FRASER A., FRANCIS L., GARNER P., GRIFFITHS M.N.D., GWILLIAM R., HALL R.E., GRAHAM D.V., GRIFFITHS C., HARRIS J.L., HEATH P.D., HO S., HOLDEN J.L., HOWDEN P.J., HAMMOND S., HARVEY J.L., HEATH P.D., HEATH P.D., HOLDEN J.L., HOWDEN P.J.,

CC

- RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Laird G.K., Knights A.M., King A., Lloyd C., Lovell J.D., Lehvaaestalo M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A., Milne S.A., Mistriy D., Moore M.J., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H., Ross M.T., Ross C.E., Scott C.E., Sherratt C.A., Sulston J.E., Rice C.D., Smith M.L., Soderlund C., Stewart C., Sulston J.E., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaughn M., Wall J.M., Williams A., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Wimling L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J.; "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414: 865-871 (2001). [5]
- RL SEQUENCE FROM N.A.
- RP TISSUE=Testis;
- RX MEDLINE=2388557; PubMed=12477932;
- RA STRAUSBERG R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Feingold F.S., Wagner L., Schulter G.D., Altachsel S.F., Zeeberg B., Buettow K.H., Schaefer C.P., Blat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullally S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Richards S., Worley K.C., Hale S., Gunaratne P.H., Villalon D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Halton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutifad G.G., Blakesley R.W., Touchman J.W., Green D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schermer A., Schein J.E., Jones S.J.M., Marras M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99: 16899-16903 (2002). [6]
- RN SEQUENCE OF 1-172 FROM N.A.
- RX MEDLINE=0122673; PubMed=10655587;
- RA BATILLE E., Sancho E., Franci C., Dominguez D., Monfar M., Baulida J., Garcia de Herreros A.; "The transcription factor Snail is a repressor of E-cadherin gene expression in epithelial tumour cells."; Nat. Cell Biol. 3:84-89 (2000).
- RL FUNCTION: SEEMS TO BE INVOLVED IN EMBRYONIC MESODERM FORMATION.
- CC BINDS TO 3 E-BOXES OF THE E-CADHERIN GENE PROMOTER AND REPRESSES ITS TRANSCRIPTION.
- CC SUBCELLULAR LOCATION: Nuclear (Potential).
- CC TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES WITH THE HIGHEST EXPRESSION IN KIDNEY.
- CC SIMILARITY: BELONGS TO THE SNAIL FAMILY OF ZINC FINGER PROTEINS.
- CC SIMILARITY: Contains 4 C2H2-type zinc fingers.
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- CC DR EMBL; AF125377; AAD173321; -
- CC DR EMBL; AJ245657; CAB52414-1; -
- CC DR EMBL; AJ245658; CAB52414-1; JOINED.
- CC DR EMBL; AJ245659; CAB52414-1; JOINED.
- CC DR EMBL; AF125233; AAD52986-1; -
- CC DR EMBL; AF177731; AAD52996-1; -
- CC DR EMBL; AL121712; CAC07340-1; -
- CC DR EMBL; BC012910; AAH12910-1; -

- DR EMBL; AF131208; AAF32527-1; -
- DR GenBank; HGNC:111128; SNAIL.
- DR MIM: 604238; -
- DR InterPro; IPR001087; Znf\_C2H2.
- DR Pfam; PF00016; 25-C2H2; 4.
- DR ProDom; PD000033; Znf\_C2H2; 1.
- DR SMART; SM00355; Znf\_C2H2; 4.
- DR PROSITE; PS00028; Zinc\_FINGER\_C2H2\_1; 3.
- DR PROSITE; PS00157; Zinc\_FINGER\_C2H2\_2; 4.
- DR Developmental protein\_Zinc-finger\_Metal-binding; DNA-binding;
- KW Nuclear protein\_Rept.
- KW C2H2-TYPE 1.
- FT ZN\_FING 154 176
- FT ZN\_FING 178 202
- FT ZN\_FING 208 230
- FT ZN\_FING 236 259
- FT CONFLICT 118 118 V->A (IN REF. 1).
- FT CONFLICT 154 154 F->S (IN REF. 6).
- SQ SEQUENCE 264 AA; 29083 MW; 70E28C9BB154115 CRC64;
- Query Match Score 40.5; DB 1; Length 264;
- Best Local Similarity 60.0%; Pred. No. 28;
- Matches 9; Conservative 4; Mismatches 1; Gaps 1;
- RESULT 11
- VG03\_BPF4 STANDARD; PRT; 176 AA.
- AC P13331; 01-JAN-1990 (Rel. 1. 13, Created)
- DB 18 NYSELQDSNPEFTQ 32
- QY 1 DYSYLYQSDPD-SFQ 14
- DB AC P13331; 01-FEB-2003 (Rel. 1. 41, Last sequence update)
- DB DT 10-OCT-2003 (Rel. 1. 42, Last annotation update)
- DB Tail\_sneath\_stabilizing\_protein\_Gp3;
- GN 3.
- DB Bacteriophage T4.
- RN Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
- OC OC TA-like viruses
- OC NCBI\_TaxID=10665;
- RN [1]
- RN SEQUENCE FROM N.A.
- RX MEDLINE=89123061; PubMed=2644202;
- RA Lipinska B., Rao A.S.M.K., Bolten B.M., Balakrishnan R., Goldberg B.B.; "Cloning and identification of bacteriophage T4 gene 2 product gp2 and action of gp2 on infecting DNA in vivo."; J. Bacteriol. 171:488-497 (1989). [2]
- RN SEQUENCE FROM N.A.
- RX MEDLINE=89296504; PubMed=2740244;
- RA Koch T., Laum N., Rueger W.; "Sequencing, cloning and overexpression of genes of bacteriophage T4" between map positions 74.25 and 77.184."; Nucleic Acids Res. 17:4392-4392 (1989). [3]
- RN SEQUENCE OF 57-143 FROM N.A.
- RX MEDLINE=86037230; PubMed=1057254;
- RA Broda J., Abelson J.; "Sequence organization and control of transcription in the bacteriophage T4 trNA region."; J. Mol. Biol. 185:545-563 (1985). [4]
- RT "Bacteriophage T4 genome."; Microbiol. Mol. Biol. Rev. 67:86-156 (2003).
- RN [5]
- RN SEQUENCE OF 57-143 FROM N.A.
- RX MEDLINE=22514363; PubMed=12626685;
- RA Miller B.S., Kutter E., Moig G., Arisaka F., Kuniawa T., Ruger W.; "Function: Involved in phage morphogenesis."; Microbiol. Mol. Biol. Rev. 67:488-525 (1993).
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 CC or send an email to license@isb-sib.ch).

CC EMBL; M23012; AAA50419\_1; -.  
 DR EMBL; AF158101; AA042496\_1; -.  
 DR EMBL; X03016; CAA26799\_1; -.  
 DR PIR; C32254; ZRBST9; -.  
 DR PIR; C32254; ZRBST9; -.

FT CONFLICT 57 63 GRAQRPG -> ASTTPVY (IN REF. 4).  
 FT CONFLICT 71 71 L -> Q (IN REF. 4).  
 FT CONFLICT 142 143 EF -> RI (IN REF. 4).  
 FT CONFLICT 176 176 V -> VILMQLFCVY (IN REF. 1).  
 SQ SEQUENCE 176 AA; 19712 MW; 34A0887DBD7D9F7P CRC4;

Query Match 48.2%; Score 40; DB 1; Length 176;  
 Best Local Similarity 60.0%; Pred. No. 21;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 Pairs 0;

Qy 1 DSYLQSDPP 10  
 Db 142 EFSXTEDSDP 151

RESULT 12  
 SUOE\_BOVIN STANDARD; PRT; 295 AA.  
 AC P19217;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Estrogen sulfotransferase (EC 2.8.2.4) (Sulfotransferase, estrogen-  
 preferring) (STR11) (PR)

GN STE OR SULTE1 OR OST.  
 OS Bos taurus (Bovine). Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Metazoa; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 NCBI\_TaxID=9913;

[1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE:Placenta;  
 RX MEDLINE=90147277; PubMed=3271383;  
 RA Nash A.R., Glenn W.K., Moore S.S., Kerr J., Thompson A.R.,  
 RA Thompson E.O.P.;  
 RT "Oestrogen sulfotransferase: molecular cloning and sequencing of cDNA  
 RT for the bovine placental enzyme.";  
 RL Aust. J. Biol. Sci. 41:507-516(1988).  
 RN PARTIAL SEQUENCE.  
 RC TISSUE:Placenta;  
 RX MEDLINE=90104087; PubMed=3270501;  
 RA Moore S.S., Thompson E.O.P., Nash A.R.;  
 RT "Oestrogen sulfotransferase: isolation of a high specific activity  
 RT species from bovine placenta.";  
 RL Aust. J. Biol. Sci. 41:333-341(1988).  
 RN [3] SEQUENCE OF 146-160 AND 206-220, AND CHARACTERIZATION.

RC TISSUE:Placenta;  
 RX MEDLINE=91152101; PubMed=1900200;  
 RA Adams J.B.;  
 RT "Enzymic synthesis of steroid sulphates. XVII. On the structure of  
 bovine estrogen sulfotransferase.";  
 RL Biochim. Biophys. Acta 107:282-288(1991).  
 CC [-] FUNCTION: May control the level of the estrogen receptor by  
 CC sulfonylating free estradiol.  
 CC [-] CATALYTIC ACTIVITY: 3'-Phosphoadenylylsulfate + estrone =  
 CC adenosine 3',5'-bisphosphate + estrone 3'-sulfate.  
 CC [-] SUBUNIT: Homodimeric.  
 CC [-] SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- INDUCTION: By progesterone.  
 CC -!- SIMILARITY: Belongs to the sulfotransferase family.  
 CC -----  
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 CC -----  
 CC EMBL; M54342; AAA30579\_1; -.  
 DR EMBL; X56335; CRA39806\_1; -.  
 DR PIR; S29045; S29045.  
 DR HSSP; P49891; LAQU.  
 DR InterPro; IPR000863; Sulfotransferase.  
 DR Pfam; PF00685; Sulfotransferase\_1.  
 DR ProDom; PD001218; Sulfotransferase\_1.  
 KW Transferase; Phosphorylation; Steroid-binding.  
 KW PHOSPHORYLATION (BY PKA) (POTENTIAL).  
 FT MOD\_RBS 216 216  
 MOD\_RBS 228 228  
 FT CONFLICT 117 117  
 FT CONFLICT 171 171 S -> E (IN REF. 2).  
 FT CONFLICT 248 248 M -> Q (IN REF. 2).  
 SQ SEQUENCE 295 AA; 34640 MW; 69147C73146913FD CRC64;

Query Match 48.2%; Score 40; DB 1; Length 295;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DPDSFQD 15  
 Db 151 DPDSFQD 157

RESULT 13  
 MYCO\_STRCI STANDARD; PRT; 550 AA.  
 ID MYCO\_STRCI P20910;  
 AC P20910;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Mycolysin precursor (EC 3.4.24.31) (Neutral metalloproteinase) (NPR)  
 DE (Pronase).  
 GN NPR.  
 OS Streptomyces cacaoi.  
 OC Streptomyceinae; Actinomycetales;  
 OC Streptomyces; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1898;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRATN-YM15;  
 RX MEDLINE=90155973; PubMed=2341042;  
 RX Chang P.-C., Kuo T.-C., Tsugita A., Lee Y.-H.W.;  
 RT "Extracellular metalloprotease gene of Streptomyces cacaoi:  
 RT structure, nucleotide sequence and characterization of the cloned  
 RT gene product.";  
 RT Gene 88:87-95 (1990).  
 RL [2]  
 RP PROCESSING, ACTIVE SITE, ZINC-LIGANDS, AND MUTAGENESIS.  
 RX MEDLINE=92156138; PubMed=1740443;  
 RX Chang P.-C., Lee Y.-H.W.;  
 RA "Extracellular autoprocessing of a metalloprotease from Streptomyces  
 RA cacaoi.";  
 RL J. Biol. Chem. 267:3952-3958(1992).  
 CC [-] CATALYTIC ACTIVITY: Preferential cleavage of bonds with  
 CC hydrophobic residues in P1.  
 CC [-] COFACTOR: Binds 1 zinc ion.  
 CC [-] SUBCELLULAR LOCATION: Secreted.  
 CC [-] SIMILARITY: Belongs to peptidase family M5.  
 CC -----  
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CC DR EMBL; M37055; AAA26789.1; - .  
 DR MEROPS; M05.001; - .  
 DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
 DR InterPro; IPR000437; Prok\_Lipoprot\_S.  
 DR PROSITE; PS00142; ZINC PROTEASE; FALSE NEG.  
 KW Hydrolase; Metalloprotease; Zinc; Zymogen; Signal.  
 FT PROPEP 1 34  
 PROPEP 35 205  
 FT CHAIN 206 550 MYCOLYSIN  
 FT METAL 407 407 ZINC (CATALYTIC).  
 FT ACT SITE 408 408 ZINC (CATALYTIC).  
 FT METAL 411 411 ZINC (CATALYTIC).  
 FT METAL 445 445 ZINC (CATALYTIC).  
 SQ SEQUENCE 550 AA; 58578 MW; C9FF9C99804D8BE CRC64;  
 Query Match 48.2%; Score 40; DB 1; Length 550;  
 Best Local Similarity 66.7%; Prod. No. 77;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 DSYLQDSDPD 12  
 Db 390 DKVHLADSDPD 401

RESULT 14  
 VG228\_BPM15 STANDARD; PRT; 595 AA.  
 ID VG228\_BPM15 STANDARD; PRT; 595 AA.  
 AC Q05235;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DE Minor tail protein GP28.  
 GN 28.  
 OS Mycobacteriophage L5.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
 OC L5-like viruses.  
 NCBI\_TaxID=31757;

RN [1] RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-8.  
 RX MEDLINE=93211282; PubMed=8459766;  
 RA Hatfull G.F.; Sarkis G.J.;  
 RT "DNA sequence, structure and gene expression of mycobacteriophage L5:  
 RT a phage system for mycobacterial genetics.";  
 RL Mol. Microbiol. 7:395-405 (1993).  
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 or send an email to license@isb-sib.ch).

CC DR PIR; Z11946; CAA71404.1; - .  
 FT INIT\_MET 0 O  
 SQ SEQUENCE 595 AA; 66759 MW; 679132A2644E9142 CRC64;  
 Query Match 48.2%; Score 40; DB 1; Length 595;  
 Best Local Similarity 50.0%; Prod. No. 84;  
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

CC DR PIR; S30973; S30973; - .  
 FT INIT\_MET 0 O  
 SQ SEQUENCE 595 AA; 66759 MW; 679132A2644E9142 CRC64;  
 Query Match 48.2%; Score 40; DB 1; Length 595;  
 Best Local Similarity 50.0%; Prod. No. 84;  
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

CC DR PIR; S30973; S30973; - .  
 FT INIT\_MET 0 O  
 SQ SEQUENCE 595 AA; 66759 MW; 679132A2644E9142 CRC64;  
 Query Match 48.2%; Score 40; DB 1; Length 595;  
 Best Local Similarity 50.0%; Prod. No. 84;  
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

RESULT 15  
 ASM\_HUMAN STANDARD; PRT; 629 AA.  
 ID ASM\_HUMAN P17406; Q13811; Q16837; Q16841;  
 AC P17406; Q13811; Q16837; Q16841;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DR Sphingomyelin phosphodiesterase precursor (EC 3.1.4.12) (Acid  
 sphingomyelinase) (asMase).  
 DE Sphingomyelinase.  
 GN Homo sapiens (Human). Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Euksaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9605;  
 RN [1] PRT SEQUENCE FROM N.A., AND ALTERNATIVE SPlicing.  
 RX MEDLINE=91217057; PubMed=1840500;  
 RA Schuchman E.H.; Suchi M.; Takahashi T.; Sandhoff K.; Desnick R.J.;  
 RT "Human acid sphingomyelinase. Isolation, nucleotide sequence and  
 RT expression of the full-length and alternatively spliced cDNAs.";  
 RT J. Biol. Chem. 266:8531-8539 (1991).  
 RN [2] PRT SEQUENCE FROM N.A.  
 RX MEDLINE=93183402; PubMed=1292508;  
 RA Newrzella D.; Stoffel W.;  
 RT "Molecular cloning of the acid sphingomyelinase of the mouse and the  
 RT organization and complete nucleotide sequence of the gene.";  
 RL Bio. Chem. Hoppe-Seyler 373:1233-1238 (1992).  
 RN [3] PRT SEQUENCE FROM N.A.  
 RX MEDLINE=92155708; PubMed=1740330;  
 RA Schuchman E.H.; Levran O.; Pereira L.V.; Desnick R.J.;  
 RT "Structural organization and complete nucleotide sequence of the gene  
 RT encoding human acid sphingomyelinase (SMPDL)." ;  
 RL Genomics 12:197-205 (1992).  
 RN [4] PRT SEQUENCE FROM N.A., AND VARIANT ARG-157.  
 RX MEDLINE=94012573; PubMed=8407668;  
 RA Ida H.; Rennert O.M.; Bto Y.; Chan W.Y.;  
 RT "Cloning of a human acid sphingomyelinase cDNA with a new mutation  
 RT that renders the enzyme inactive.";  
 RL J. Biochem. 114:15-20 (1993).  
 RN [5] PRT SEQUENCE OF 128-629 FROM N.A., PARTIAL SEQUENCE, AND  
 ALTERNATIVE SPlicing.  
 RP TISSUE\_Fibroblast  
 RC CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=9060003; PubMed=2555181;  
 RA Reinkel L.E.; Schuchman E.H.; Levran O.; Suchi M.; Ferlinz K.,  
 RA Reinkel H.; Sandhoff K.; Desnick R.J.;  
 RT "Isolation of cDNA clones encoding human acid sphingomyelinase:  
 RT occurrence of alternatively processed transcripts.";  
 RL EMBO J. 8:2469-2473 (1989).  
 RN [6] PRT DISULFIDE BONDS  
 RX MEDLINE=22518502; PubMed=12631268;  
 RA Lansmann S.; Schuette C.G.; Bartelsen O.; Hoernschmeyer J.; Linker T.,  
 RA Weisgerber J.; Sandhoff K.;  
 RT "Human acid sphingomyelinase.";  
 RA Eur. J. Biochem. 270:1076-1088 (2003).  
 RN [7] PRT VARIANT\_NPA SER-577.  
 RX MEDLINE=92028849; PubMed=1718266;  
 RA Ferlinz K.; Hurwitz R.; Sandhoff K.;  
 RT "Molecular basis of acid sphingomyelinase deficiency in a patient

- with Niemann-Pick disease type A.";
- RL Biochem. Biophys. Res. Commun. 173:1187-1191(1991).
- RN [9] VARIANT NPA LEU-496; PubMed=2023926;
- RP VARIANT NPA TYR-449; PubMed=12340429; PMID=12340429; PubMed=12340429; MEDLINE=12340429; Variant NPA TYR-449.
- RX Levran O., Desnick R.J., Schuchman E.H.; "Niemann-Pick disease: a frequent missense mutation in the acid sphingomyelinase gene of Ashkenazi Jewish type A and B patients.";
- RA Levran O., Desnick R.J., Schuchman E.H.; "Niemann-Pick type B disease. Identification of a single codon deletion in the acid sphingomyelinase gene and genotype/phenotype correlations in type A and B patients.";
- RT Levran O., Desnick R.J., Schuchman E.H.; "Identification and expression of a common missense mutation (I302P) in the acid sphingomyelinase gene of Ashkenazi Jewish type A patients.";
- RN [10] VARIANT NPA ARG-608 DEL; MEDLINE=91358737; PubMed=1885770;
- RP VARIANT NPA PRO-302; MEDLINE=91040773; PubMed=1391960;
- RT Levran O., Desnick R.J., Schuchman E.H.; "Identification and expression of a common missense mutation (I302P) in the acid sphingomyelinase patients.";
- RL Blood 80:2081-2087(1992).
- RP VARIANT NPB ARG-436; MEDLINE=33244334; PubMed=1301192;
- RP VARIANT NPA ILE-382; AND VARIANT NPB ARG-242 AND SER-383. MEDLINE=9316934; PubMed=1618760;
- RA Takahashi T., Desnick R.J., Takada G., Schuchman E.H.; "Identification of a missense mutation (S43GR) in the acid sphingomyelinase gene from a Japanese patient with type B Niemann-Pick disease.";
- RT Takahashi T., Suchi M., Desnick R.J., Takada G., Schuchman E.H.; "Identification and expression of five mutations of five mutations in the human acid sphingomyelinase gene causing types A and B Niemann-Pick disease."
- RT Molecular evidence for genetic heterogeneity in the neuronopathic and non-neuronopathic forms.";
- RL Hum. Mutat. 1:70-71(1992).
- RP VARIANT NPB GLY-391; MEDLINE=94328611; PubMed=8051942;
- RA Sperli W., Bart G., Vanier M.T., Christomano H., Baldissera I., Stechensdorf F., Pasche B.; "A family with visceral course of Niemann-Pick disease, macular halo syndrome and low sphingomyelin degradation rate.";
- RT Niemann-Pick disease: N389T and R441X.";
- RL Hum. Mutat. 6:1352-1354(1995).
- RP VARIANT NPA CYS-446; MEDLINE=16274768; PubMed=8693491;
- RA Takahashi T., Suchi M., Sato W., Ten S. B., Sakuragawa N., Desnick R.J., Schuchman E.H., Takeda G.; "Identification and expression of a missense mutation (Y446C) in the acid sphingomyelinase gene from a Japanese patient with type A Niemann-Pick disease.";
- RT Niemann-Pick disease.";
- RL Tonoku J. Exp. Med. 177:117-123(1995).
- RP VARIANT NPA GLN-246; MEDLINE=96263741; PubMed=8664904;
- RA Ida H., Rennert O.M., Maekawa K., Eto Y.; "Identification of three novel mutations in the acid sphingomyelinase gene of Japanese patients with Niemann-Pick disease type A and B.";
- RL Hum. Mutat. 7:65-67(1996).
- RN [18] VARIANT NPB TYR-421; MEDLINE=12340429; PubMed=12340429; Variant NPB TYR-421.
- RP VARIANT NPB SER-371; AND ARG-608; MEDLINE=12444008; PubMed=12444008; Variant NPB SER-371; AND ARG-608.
- RA Schuchman E.H.; "The demographics and distribution of type B Niemann-Pick disease: novel mutations lead to new genotype/phenotype correlations.";
- RT Am. J. Hum. Genet. 71:1413-1419(2002).
- RN [19] VARIANT NPA ARG-248; TYR-319; SER-463; LEU-475 AND HIS-537, AND RP VARIANT NPB SER-371; AND ARG-608; Variant NPB SER-371; AND ARG-608.
- RX Sikora J., Pavlus-Pereira H., Ellieder M., Roelofs H., Wevers R.A.; "Seven novel Acid sphingomyelinase gene mutations in Niemann-Pick type A and B patients.";
- RT Ann. Hum. Genet. 67:63-70(2003).
- CC -|- FUNCTION: Converts sphingomyelin to ceramide. ASM also has phospholipase C activities toward 1,2-diacylglycerol sphingomyelinase and 1,2-diacylglycerol sphingomyelin + H(2)O = N-acylsphingosine + choline phosphate.
- CC -|- CATALYTIC ACTIVITY: Spingomyelin + H(2)O = N-acylsphingosine + choline phosphate.
- CC -|- SUBUNIT: Monomer.
- CC -|- SUBCELLULAR LOCATION: Lysosomal.
- CC -|- ALTERNATIVE PRODUCTS:
- CC -|- Event=Alternative splicing; Named isoforms=3;
- CC -|- Name=1; Synonyms=ASM-1;
- CC -|- IsoId=P17405-1; Sequence=Displayed;
- CC -|- Name=2; Synonyms=ASM-2;
- CC -|- IsoId=P17405-2; Sequence=VSP\_000331; VSP\_000332; Name=3; Synonyms=ASM-3;
- CC -|- IsoId=P17405-3; Sequence=VSP\_000333;
- CC -|- DISBASE: Defects in SMPD1 are the cause of Niemann-Pick disease type A (NPA) [MIM:257200]; also referred to as the classical infantile form. Niemann-Pick disease is a clinically and genetically heterogeneous recessive disorder. It is caused by the accumulation of sphingomyelin and other metabolically related lipids in the lysosomes, resulting in neurodegeneration starting from early life. Patients may show xanthomas, pigmentation, hepatosplenomegaly, lymphadenopathy and mental retardation. Niemann-Pick disease occurs more frequently among individuals of Ashkenazi Jewish ancestry than in the general population. NPA is characterized by very early onset in infancy and a rapidly progressive course leading to death by three years.
- CC -|- DISBASE: Defects in SMPD1 are the cause of Niemann-Pick disease type B (NPB) [MIM:607616]; also referred to as the visceral form. NPB has little if any neurologic involvement and patients may survive into adulthood.
- CC -|- MISCELLANEOUS: There are two types of sphingomyelinases: ASM (acid), and NSM (neutral). Isoform 1 is the most abundant (90%), isoforms 2 (10%) and 3 (<1%) are only found at lower levels. Only isoform 1 is a catalytic active enzyme.
- CC -|- SIMILARITY: Belongs to the acid sphingomyelinase family.
- CC -|- SIMILARITY: Contains 1 saposin B-type domain.
- CC -|- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the European Molecular Biology Laboratory.
- Query Match Score 40; DB 1; Length 629;
- Best Local Similarity 54.5%; Pred. No. 90;
- Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
- Qy 1 DYSYLDSDPD 11
- Db 210 DHDXLEGTPDP 220
- Search completed: June 3, 2004, 15:14:46
- Job time : 11 secs

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## OM protein - protein search, using SW model

Run on: June 3, 2004, 15:09:24 ; Search time 36.5 Seconds

(without alignments)

129.665 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_448\_462  
Perfect score: 83  
Sequence: 1 DSYLQNSDPDSFQD 15Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : SPTRMBL25:\*

1: sp\_archea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_micr:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rhodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_virus:\*

16: sp\_bacteriap:\*

17: sp\_archeap:\*

17 17 75 90.4 135 6 Q9GLS3

18 18 73 88.0 135 6 Q8WMS6

19 19 73 88.0 135 6 Q8MTU6

20 20 72 86.7 135 6 Q9GLUT7

21 21 71 85.5 135 6 Q9MFT7

22 22 68 81.9 135 6 Q9GLV3

23 23 68 81.9 135 6 Q9GRM9

24 24 68 81.9 135 6 Q9GLT9

25 25 68 81.9 135 6 Q9GLT7

26 26 68 81.9 135 6 Q9GRK5

27 27 68 81.9 135 6 Q9Gm7

28 28 54 65.1 533 11 Q91XK0

29 29 51 61.4 530 6 Q7YRB8

30 30 49 59.0 308 11 Q8CJ7

31 31 49 59.0 336 17 Q283T7

32 32 49 59.0 353 4 Q8Y68

33 33 48 57.8 696 4 Q96SP9

34 34 48 57.8 696 1 Q810C1

35 35 48 57.8 760 4 Q96PP8

36 36 46 55.4 340 4 Q8N9T8

37 37 45 54.2 232 16 Q8XH15

38 38 45 54.2 309 16 Q8CTQ2

39 39 45 54.2 393 16 Q92eb8

40 40 45 54.2 393 16 Q8YJ0

41 41 45 54.2 476 10 Q9STB2

42 42 45 54.2 476 10 Q8lfq0

43 43 45 54.2 527 13 Q9PST0

44 44 45 54.2 529 13 Q91436

45 45 54.2 529 13 Q8UU5

## ALIGNMENTS

RESULT 1  
Q15677  
ID Q15677  
AC Q15677;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DB Tyrosinase-related gene segment, exon 5 (Fragment).  
Homo sapiens (Human).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Buteraria; Primates; Catarrhini; Hominoidea; Homo.  
CX NCBI TaxID=9606;  
RN [1] \_  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91236163; PubMed=1903356;  
RA Giebel, L.B., Strunk, K.M., Spritz, R.A.;  
RT "Organization and nucleotide sequences of the human tyrosinase gene  
and a truncated tyrosinase-related segment.";  
RT and a truncated tyrosinase-related segment.";  
RL Genomics 9:435-445(1991).  
DR EMBL; M63241; AAA73001..1;  
DR EMBL; M63240; AAA73001..1;  
DR GO; GO:006491; P:oxidoreductase activity; IEA.  
DR InterPro; IPR008922; Di-copper centre.  
DR InterPro; IPR002227; Tyrcoinase.  
PFam; PF00264; Tyrosinase; 1.  
FT NON\_TER  
SQ SEQUENCE 134 AA; 15770 MW; 7438E1B6B960DB9A CRC64;  
Query Match 100.0% Score 83; DB 4; Length 134;  
Best Local Similarity 100.0% Pred. No. 3.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Score Query Match Length DB ID Description

1 83 100.0 134 4 Q15677

2 83 100.0 134 6 Q9GLU9

3 83 100.0 134 6 Q9GLU5

4 83 100.0 134 6 Q9GLS9

5 83 100.0 135 6 Q9GLU1

6 83 100.0 135 6 Q9GLU3

7 83 100.0 529 6 Q9BDE0

8 78 94.0 134 6 Q9GLT1

9 75 90.4 135 6 Q9GLT3

10 75 90.4 135 6 Q9GLR7

11 75 90.4 135 6 Q9GLS5

12 75 90.4 135 6 Q9GLV1

13 75 90.4 135 6 Q9GLR9

14 75 90.4 135 6 Q9GLS1

15 75 90.4 135 6 Q9GLT5

16 75 90.4 135 6 Q9GLS7

1 DYSYIQLSDPDSFQD 15

53 DYSYIQLSDPDSFQD 67

OY

DB

RESULT 2

Q9GLU9	PRELIMINARY;	PRT;	134 AA.
ID Q9GLU9;			
AC Q9GLU9;			
DT 01-MAR-2001 (TREMBLrel. 16, Created)			
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE Tyrosinase (EC 1.14.18.1) (Fragment).			
OS Pan troglodytes (Chimpanzee).			
OC Bokaryota; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Primates; Catarrhini; Hominidae; Pan.			
OX NCBI_TaxID=9598;			
RN [1]			
RP FROM N.A.			
RA Ding B., Ryder O.A., Shi P., Zhang Y.-P., i			
RT "Molecular evolution of tyrosinase gene in primates.";			
RL Submitted -1999 (SEP-1999) to the EMBL/GenBank/DBJ databases.			
DR EMBL; AF133592; AAGG6323.1; -;			
DR EMBL; AF133591; AAGG6323.1; JOINED.			
DR GO; GO:00016491; F:monophenol monooxygenase activity; IEA.			
DR GO; GO:0008152; P:metabolism; IEA.			
DR InterPro; IPR008922; Di-copper_centre.			
DR InterPro; IPR002227; Tyrosinase.			
DR Pfam; PF00264; tyrosinase; 1.			
KW Oxidoreductase.			
FT NON TER 1 1			
SQ SEQUENCE 134 AA; 15754 MW; 7428A1BAF97CDB9A CRC64;			

Query Match Score 83; DB 6; Length 134;  
Best Local Similarity 100.0%; Pred. No. 3.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYLOQSDPPSFQD 15

Db 53 DYSYLOQSDPPSFQD 67

---

RESULT 3

Q9GLU5	PRELIMINARY;	PRT;	134 AA.
ID Q9GLU5;			
AC Q9GLU5;			
DT 01-MAR-2001 (TREMBLrel. 16, Created)			
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE Tyrosinase (EC 1.14.18.1) (Fragment).			
OS Gorilla gorilla (gorilla).			
OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Gorilla.			
OX NCBI_TaxID=9593;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Ding B., Ryder O.A., Shi P., Zhang Y.-P., i			
RT "Molecular evolution of tyrosinase gene in primates.";			
RL Submitted -1999 (SEP-1999) to the EMBL/GenBank/DBJ databases.			
DR EMBL; AF13663; AAGG2722.1; -;			
DR EMBL; AF13602; AAGG2722.1; JOINED.			
DR GO; GO:00016491; F:monophenol monooxygenase activity; IEA.			
DR GO; GO:0008152; P:metabolism; IEA.			
DR InterPro; IPR002227; Tyrosinase.			
DR InterPro; IPR002222; Tyrosinase.			
DR Pfam; PF00264; tyrosinase; 1.			
KW Oxidoreductase.			
FT NON TER 1 1			
SQ SEQUENCE 134 AA; 15754 MW; 7428A1BAF97CDB9A CRC64;			

Query Match Score 83; DB 6; Length 134;  
Best Local Similarity 100.0%; Pred. No. 3.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYLOQSDPPSFQD 15

1 DYSYIQLQSDPDSFQD 15  
 | :|:|:|:|:|:|:|:  
 QY 53 DYSYIQLQSDPDSFQD 67

RESULT 6  
 ID Q9GLU3 PRELIMINARY; PRT; 135 AA.  
 AC Q9GLU3;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 OS Hylobates hoolock (Hoolock gibbon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.  
 OX NCBI\_TaxID=61851;  
 RN [1] SEQUENCE FROM N.A.  
 RP Ding B.; Ryder O.A.; Shi P.; Zhang Y.-P.;  
 RA RT "Molecular evolution of tyrosinase gene in primates."  
 RL Submitted (Sep-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF183608; AAG28343.1; -.  
 DR EMBL; AF183607; AAC28343.1; JOINED.  
 DR GO; GO:0016491; F:monophenol monooxygenase activity; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR008922; Di-copper\_centre.  
 DR Pfam; PF00264; tyrosinase; 1.  
 KW Oxidoreductase.  
 FT NON\_TER 1 15857 MW; AA12FCE/2BF5866B CRC64;  
 SQ SEQUENCE 135 AA; 15857 MW; AA12FCE/2BF5866B CRC64;

Query Match 100.0%; Score 83; DB 6; Length 135;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYIQLQSDPDSFQD 15  
 Db 53 DYSYIQLQSDPDSFQD 67

RESULT 7  
 ID Q9BDE0 PRELIMINARY; PRT; 529 AA.  
 AC Q9BDE0;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Tyrosinase.  
 OS Gorilla gorilla (gorilla).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.  
 OX NCBI\_TaxID=9593;  
 RN [1] SEQUENCE FROM N.A.  
 RP STRAIN-Snowflake, Ndengue, and Machinda;  
 RC Martinez-Arias R.; Comas D.; Bertranpetti J.;  
 RA "Tyrosinase gene in gorilla and the albinism of Snowflake."  
 RT Submitted (Feb-2000) to the EMBL/GenBank/DDBJ databases.  
 RL EMBL; AF237806; AAK00804.1; -.  
 DR EMBL; AF237802; AAK00804.1; JOINED.  
 DR EMBL; AF237803; AAK00804.1; JOINED.  
 DR EMBL; AF237804; AAK00804.1; JOINED.  
 DR EMBL; AF237805; AAK00804.1; JOINED.  
 DR EMBL; AF237796; AAK00802.1; -.  
 DR EMBL; AF237792; AAK00802.1; JOINED.  
 DR EMBL; AF237793; AAK00802.1; JOINED.  
 DR EMBL; AF237794; AAK00802.1; JOINED.  
 DR EMBL; AF237795; AAK00802.1; JOINED.  
 DR EMBL; AF237801; AAK00803.1; -.

Query Match 100.0%; Score 83; DB 6; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYIQLQSDPDSFQD 15  
 Db 448 DYSYIQLQSDPDSFQD 462

RESULT 8  
 ID Q9GLT1 PRELIMINARY; PRT; 134 AA.  
 AC Q9GLT1;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Tyrosinase (EC 1.14.18.1) (Fragment).  
 OS Pongo pygmaeus (Orangutan).  
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.  
 OX NCBI\_TaxID=9600;  
 RN [1] SEQUENCE FROM N.A.  
 RP Ding B.; Ryder O.A.; Shi P.; Zhang Y.-P.;  
 RA RT "Molecular evolution of tyrosinase gene in primates."  
 RL Submitted (Sep-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF183648; AA227278.1; -.  
 DR EMBL; AF183647; AA227278.1; JOINED.  
 DR GO; GO:00054503; F:monophenol monooxygenase activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR002227; Tyrosinase.  
 DR Pfam; PF00264; tyrosinase; 1.  
 KW Oxidoreductase.  
 FT NON\_TER 1 15823 MW; 1E83D060520CDDB9B CRC64;  
 SQ SEQUENCE 134 AA; 15823 MW; 1E83D060520CDDB9B CRC64;

Query Match 100.0%; Score 78; DB 6; Length 134;  
 Best Local Similarity 93.3%; Pred. No. 2.2e-05;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYSYIQLQSDPDSFQD 15  
 Db 53 DYSYIQLQSDPDSFQD 67

RESULT 9  
 ID Q9GLT3 PRELIMINARY; PRT; 135 AA.  
 AC Q9GLT3;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Tyrosinase (EC 1.14.18.1) (Fragment).	Q9GLS5; PRELIMINARY; PRT; 135 AA.
OS Nasalis larvatus (Proscocidae monkey).	AC Q9GLS5; DT 01-MAR-2001 (TREMBLrel. 16, Created)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
OC Nasalis.	DE Tyrosinase (EC 1.14.18.1) (Fragment)
OX NCBI_TaxID=43780;	OS Trachypithecus phayrei (Phayre's leaf monkey).
RN [1]	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RP SEQUENCE FROM N.A.	OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;	OC Trachypithecus.
RT Molecular evolution of tyrosinase gene in primates.";	OC NCBI_TaxID=61618;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.	RN [1]
DR EMBL; AF181643; AAG27275.1; -.	RP SEQUENCE FROM N.A.
DR EMBL; AF183642; AAG27275.1; JOINED.	RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;
DR GO; GO:0016491; F:monophenol monooxygenase activity; IEA.	RT "Molecular evolution of tyrosinase gene in primates.";
DR GO; GO:0016491; F:oxidoreductase activity; IEA.	RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR GO; GO:0016491; F:metabolism; IEA.	EMBL; AF181668; AAG29588.1; -.
DR GO; GO:0016491; P:metabolism; IEA.	DR EMBL; AF183667; AAG29588.1; JOINED.
DR InterPro; IPR008922; Di-copper centre.	GO; GO:0004503; F:monophenol monooxygenase activity; IEA.
DR InterPro; IPR002227; Tyrosinase.	DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR Pfam; PF00264; Tyrosinase; 1.	DR GO; GO:0008152; P:metabolism; IEA.
KW Oxidoreductase.	DR InterPro; IPR008922; Di-copper centre.
FT NON TER	DR InterPro; IPR002227; Tyrosinase; 1.
SQ SEQUENCE 135 AA; 15690 MW; FE9070222D41PA88 CRC64;	DR Pfam; PF00264; tyrosinase; 1.
Query Match 90.4%; Score 75; DB 6; Length 135;	DR FT NON TER 1 15656 MW; FE9070225962C41EB8 CRC64;
Best Local Similarity 93.3%; Pred. No. 7.3e-05;	DR SQ 135 AA; 15656 MW; FE9070225962C41EB8 CRC64;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	DR DB 53 DYSYLOQSDSDSFQD 15
Qy 1 DYSYLOQSDSDSFQD 15	DR Qy 1 DYSYLOQSDSDSFQD 15
Db 53 DYSYLOQSDSDSFQD 67	DR Db 53 DYSYLOQSDSDSFQD 67
RESULT 10	RESULT 12
Q9GLR7 PRELIMINARY; PRT; 135 AA.	Q9GLV1 PRELIMINARY; PRT; 135 AA.
AC Q9GLR7; PRELIMINARY; PRT; 135 AA.	AC Q9GLV1; PRELIMINARY; PRT; 135 AA.
DT 01-MAR-2001 (TREMBLrel. 16, Created)	AC Q9GLV1; PRELIMINARY; PRT; 135 AA.
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)	DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)	DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE Tyrosinase (EC 1.14.18.1) (Fragment).	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
OS Pygathrix bieri (Black snub-nosed monkey) (Rhinopithecus bieri);	DE Tyrosinase (EC 1.14.18.1) (Fragment).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OS Papio hamadryas (Hamadryas baboon).
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Pygathrix.	OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OX NCBI_TaxID=61621;	OC NCBI_TaxID=9557;
RN	RN [1]
RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;	RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;
RT "Molecular evolution of tyrosinase gene in primates.";	RT "Molecular evolution of tyrosinase gene in primates.";
RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.	RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF183688; AAG33663.1; -.	DR EMBL; AF183587; AAG21893.1; -.
DR GO; GO:0016491; F:monophenol monooxygenase activity; IEA.	DR EMBL; AF183586; AAG21893.1; JOINED.
DR GO; GO:0001512; F:metabolism; IEA.	DR GO; GO:0004503; F:monophenol monooxygenase activity; IEA.
DR InterPro; IPR008922; Di-copper centre.	DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR002227; Tyrosinase.	DR InterPro; IPR008922; Di-copper centre.
FT NON TER	DR FT NON TER 1 15686 MW; FE90643B963855E8 CRC64;
SQ SEQUENCE 135 AA; 15686 MW; FE90643B963855E8 CRC64;	DR SQ 135 AA; 15686 MW; FE90643B963855E8 CRC64;
Query Match 90.4%; Score 75; DB 6; Length 135;	DR FT NON TER 1 15685 MW; EBD1103B963855E8 CRC64;
Best Local Similarity 93.3%; Pred. No. 7.3e-05;	DR SQ 135 AA; 15685 MW; EBD1103B963855E8 CRC64;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	DR DB 53 DYSYLOQSDSDSFQD 15
Qy 1 DYSYLOQSDSDSFQD 15	DR Qy 1 DYSYLOQSDSDSFQD 15
Db 53 DYSYLOQSDSDSFQD 67	DR Db 53 DYSYLOQSDSDSFQD 67
RESULT 11	Q9GLS5
Q9GLS5; PRELIMINARY; PRT; 135 AA.	Q9GLS5; PRELIMINARY; PRT; 135 AA.
AC Q9GLS5; PRELIMINARY; PRT; 135 AA.	AC Q9GLS5; PRELIMINARY; PRT; 135 AA.
DT 01-MAR-2001 (TREMBLrel. 16, Created)	DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Tyrosinase (EC 1.14.18.1) (Fragment).	DE Tyrosinase (EC 1.14.18.1) (Fragment).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OS Papio hamadryas (Hamadryas baboon).
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Pygathrix.	OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OX NCBI_TaxID=61621;	OC NCBI_TaxID=9557;
RN	RN [1]
RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;	RA Ding B., Ryder O.A., Shi P., Zhang Y.-P.;
RT "Molecular evolution of tyrosinase gene in primates.";	RT "Molecular evolution of tyrosinase gene in primates.";
RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.	RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF183688; AAG33663.1; -.	DR EMBL; AF183587; AAG21893.1; -.
DR GO; GO:0016491; F:monophenol monooxygenase activity; IEA.	DR EMBL; AF183586; AAG21893.1; JOINED.
DR GO; GO:0001512; F:metabolism; IEA.	DR GO; GO:0004503; F:monophenol monooxygenase activity; IEA.
DR InterPro; IPR008922; Di-copper centre.	DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR002227; Tyrosinase.	DR InterPro; IPR008922; Di-copper centre.
FT NON TER	DR FT NON TER 1 15686 MW; FE90643B963855E8 CRC64;
SQ SEQUENCE 135 AA; 15686 MW; FE90643B963855E8 CRC64;	DR SQ 135 AA; 15686 MW; FE90643B963855E8 CRC64;
Query Match 90.4%; Score 75; DB 6; Length 135;	DR FT NON TER 1 15685 MW; EBD1103B963855E8 CRC64;
Best Local Similarity 93.3%; Pred. No. 7.3e-05;	DR SQ 135 AA; 15685 MW; EBD1103B963855E8 CRC64;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	DR DB 53 DYSYLOQSDSDSFQD 15
Qy 1 DYSYLOQSDSDSFQD 15	DR Qy 1 DYSYLOQSDSDSFQD 15
Db 53 DYSYLOQSDSDSFQD 67	DR Db 53 DYSYLOQSDSDSFQD 67
RESULT 11	Q9GLS5

Db	53 DYSYIQLQSDSDSFQD	67	Best Local Similarity 93.3%; Pred. No. 7.3e-05; Mismatches 1; Indels 0; Gaps 0;
RESULT 13			
ID Q9GLR9	PRELIMINARY;	PRT; 135 AA.	
AC Q9GLR9_	16, Created)		
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE Tyrosinase (EC 1.14.18.1) (Fragment).			
OS Trachypithecus leucocepsalus.			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Trachypithecus.			
OC NCBI_TaxID=61517;			
RN [1]	SEQUENCE FROM N.A.		
RP Ding B.; Ryder O.A.; Shi P.; Zhang Y.-P.;			
RT "Molecular evolution of tyrosinase gene in primates.";			
RL Submitted (SEP-1999) to the BMBL/GenBank/DBJ databases.			
DR EMBL; AF133683; AAG33681.1; -.			
DR EMBL; AF133682; AAG33681.1; JOINED.			
DR GO; GO:0044503; F:monophenol monooxygenase activity; IEA.			
DR GO; GO:0016491; F:oxidoreductase activity; IEA.			
DR GO; GO:0008152; P:metabolism; IEA.			
DR InterPro; IPR008922; Di-copper centre.			
DR InterPro; IPR002227; Tyrosinase.			
DR Pfam; PF0264; tyrosinase; 1.			
KW Oxidoreductase.			
FT NON TER	1		
SQ SEQUENCE 135 AA;	15656 MW;	FE90702F962C41E8 CRC64;	
Query Match	90.4%;	Score 75; DB 6; Length 135;	
Best Local Similarity 93.3%; Pred. No. 7.3e-05; Mismatches 0; Indels 0; Gaps 0;			
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Db	53 DYSYIQLQSDSDSFQD	67	0;
RESULT 14			
ID Q9GLS1	PRELIMINARY;	PRT; 135 AA.	
AC Q9GLS1_	16, Created)		
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DB Tyrosinase (EC 1.14.18.1) (Fragment).			
OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).			
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae; Trachypithecus.			
OC NCBI_TaxID=54180;			
RN [1]	SEQUENCE FROM N.A.		
RP Ding B.; Ryder O.A.; Shi P.; Zhang Y.-P.;			
RT "Molecular evolution of tyrosinase gene in primates.";			
RL Submitted (SEP-1999) to the BMBL/GenBank/DBJ databases.			
DR EMBL; AF133678; AAG33679.1; JOINED.			
DR GO; GO:0044503; F:monophenol monooxygenase activity; IEA.			
DR GO; GO:0016491; F:oxidoreductase activity; IEA.			
DR InterPro; IPR008922; Di-copper centre.			
DR InterPro; IPR002227; Tyrosinase.			
DR Pfam; PF0264; tyrosinase; 1.			
KW Oxidoreductase.			
FT NON TER	1		
SQ SEQUENCE 135 AA;	15656 MW;	FE90702F962C41E8 CRC64;	
Query Match	90.4%;	Score 75; DB 6; Length 135;	
Best Local Similarity 93.3%; Pred. No. 7.3e-05; Mismatches 1; Indels 0; Gaps 0;			
Db	53 DYSYIQLQSDSDSFQD	67	0;
RESULT 15			
QY 1 DYSYIQLQSDSDSFQD	15	PRELIMINARY;	PRT; 135 AA.
DB 53 DYSYIQLQSDSDSFQD	67		
QY 1 DYSYIQLQSDSDSFQD	15		
DB 53 DYSYIQLQSDSDSFQD	67		
Search completed: June 3, 2004, 15:14:11			
Job time : 36.5 secs			
RP Sequence	14;	Conservative 0; Mismatches 1;	Score 75; DB 6; Length 135;
Matches 14; Conservative 0; Mismatches 1;			
Db	53 DYSYIQLQSDSDSFQD	67	0;



SQ Sequence 15 AA;

Query Match 100.0%; Score 83; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYIQLDSDPDSFQD 15  
Db 1 DYSYIQLDSDPDSFQD 15

RESULT 2  
AY33169 ID AAY33169 standard; peptide; 15 AA.  
XX AC AAY33169;  
XX DT 17-NOV-1999 (first entry)  
XX DE Human tyrosinase peptide #8.  
XX KW Human; protein delivery; Yersinia sp; effector gene; mutant; antigen;  
KW immune response; cytotoxic T-lymphocyte; CTL; vaccination; treatment;  
KW pathological disorder; tyrosinase.  
XX OS Homo sapiens.  
XX PN WO945098-A2.  
XX PD 10-MAR-1999.  
XX PF 03-MAR-1999; 99WO-1B000587.  
XX PR 06-MAR-1998; 98US-00036582.  
XX PA (VBRU/) VAN DER BRUGGEN P B.  
PA (CORN/) CORNELIS G R.  
PA (BOLA/) BOLAND A M.  
PA (BOON/) BOON-FALLEUR T R.  
PI Van Der Bruggen PB, Cornelis GR, Boland AM, Boon-Falleur TR,  
XX DR WPI; 1999-540840/45.

PT New mutant Yersinia strains useful for treating a pathological disorder.  
XX Example 1 ; Page 70; 80pp; English.

CC This invention describes a novel mutant Yersinia (Y1) strain, comprising  
CC mutation(s) in effector-encoding gene(s) and deficient in the production  
CC of functional effector protein(s). The invention describes (1) a  
CC quintuple mutant Yersinia strain, having the designation Yersinia  
CC enterocolitica yopBHAQJ or Yersinia pseudotuberculosis yopBHAQJ; (2) an  
CC expression vector (EV1) for delivering a heterologous protein into a  
CC eukaryotic cell, comprising in the 5'-3' direction; (3) a Yersinia or  
CC mutant Yersinia strain for delivering a heterologous protein into a  
CC eukaryotic cell, comprising contacting the cell with a Y1 transformed  
CC with the above vector (Y1-EV1); (4) a method for delivering a  
CC heterologous protein into a eukaryotic cell, comprising contacting the  
CC cell with a Y1 transformed with the above vector (Y1-EV1); (5) a method  
CC for inducing an immune response specific for a heterologous protein; (6)  
CC for a heterologous protein; (7) a method for determining the efficacy of  
CC an antigen vaccination regimen in a subject. Y1 is used to treat a  
CC pathological disorder, by providing recombinant Yersinia for the safe  
CC delivery of proteins into eukaryotic cells. AAV33147-Y33178 are human-  
CC derived peptides used to illustrate the method of the invention  
XX Sequence 15 AA;

Qy 1 DYSYIQLDSDPDSFQD 15  
Db 1 DYSYIQLDSDPDSFQD 15

RESULT 3  
AY00711 ID AAY00711 standard; peptide; 15 AA.  
XX AC AAY00711;  
XX DT 12-MAY-1999 (first entry)  
DE Tumour antigen booster peptide Tyrosinase HLA-DR4.  
XX KW Tumour antigen; booster peptide; immune response modulation; allergy;  
KW immune response enhancer; tumour cell; tumour rejection antigen;  
KW leukocyte antigen-presenting molecule; autoimmune disease;  
KW allograft rejection.  
XX OS Homo sapiens.  
XX PN WO9858956-A2.  
XX PD 30-DEC-1998.  
XX PF 19-JUN-1998; 98NO-US012894.  
XX PR 23-JUN-1997; 970S-00880979.  
XX PA (LUDW-) LUDWIG INST CANCER RES.  
XX PI Warnier G, Uyttenhove C, Boon-Falleur T;  
XX DR WPI; 1999-105612/09.  
XX PT Immunization methods using viruses expressing antigen for priming and  
PT booster immunizations - useful for modulating immune responses against  
PT antigen, e.g. enhancing immune response against tumour cells expressing  
PT tumour rejection antigens.  
XX Disclosure; Page 9; 33pp; English.  
XX This sequence represents a tumour antigen booster peptide that can be  
CC used in the method of the invention. The method is for modulating an  
CC immune response in a mammal against an antigen, and comprises: (A)  
CC inducing an immune response by: (i) administering a virus containing a  
CC nucleic acid molecule encoding the antigen or its precursor to generate  
CC an immune response; and (ii) administering at least one booster dose  
CC comprising a peptide including the antigen, in an adjuvant, in a combined  
CC amount effective to enhance the initial immune response; or (B) reducing  
CC an immune response as defined for (A) but using a non-adjuvant with the  
CC peptide which includes the antigen, in an amount effective to reduce the  
CC initial immune response. Method (A) is used to enhance the immune  
CC response against tumour cells expressing tumour rejection antigens, and  
CC against pathogens in subjects having human leukocyte antigen-presenting  
CC molecules. Method (B) is used to reduce the immune response in allergy,  
CC autoimmune disease, and allograft rejection. Method (A) provides an  
CC immunisation method which, unlike prior art, is not limited by the host  
XX Sequence 15 AA;

Query Match 100.0%; Score 83; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYIQLDSDPDSFQD 15  
Db 1 DYSYIQLDSDPDSFQD 15

**RESULT 4**  
 AAY49659 standard; peptide; 15 AA.  
 AC AAY49659;  
 XX DT 14-JAN-2000 (first entry)  
 DE Tumour antigenic peptide SEQ ID NO:26.  
 XX Human; sdp3.10; SAGE; sdp3.8; HAGE; sdp3.5; TRAP; sarcoma;  
 KW tumour rejection antigen precursor; tumour associated nucleic acid;  
 KW carcinoma; cancer; immune response; diagnosis.  
 OS Synthetic.

XX PN WO953061-A2.  
 XX PD 21-OCT-1999.  
 XX PF 14-APR-1999; 99WO-US008163.  
 XX PR 15-APR-1998; 98US-00060706.  
 PR 27-JUL-1998; 98US-00122989.  
 PR 30-OCT-1998; 98US-00133706.  
 PR 30-OCT-1998; 98US-00183789.  
 XX PA (LUDWIG) LUDWIG INST CANCER RES.  
 XX PI Martelange V, De Smet C, Boon-Falleur T;  
 XX DR 1999-620430/53.

PT New nucleic acid encoding sarcoma-associated gene products, useful for  
 PT diagnosing, e.g. treating and preventing cancer.  
 XX Disclosure; Page 25; 93pp; English.  
 PS The present invention describes sarcoma-associated gene products (I).  
 CC Agents, specifically sarcoma associated nucleic acids (II) or their  
 CC expression products that are tumour rejection antigens (TRA), that  
 CC selectively increase formation of HLA (human leucocyte antigen) (I)  
 CC complexes are used for treating cancer, especially sarcoma and carcinoma,  
 CC in humans and other animals. Compositions containing autologous cytolytic  
 CC T cells (CTL), specific for the HLA(I) complex, are similarly useful,  
 CC also transformed cells that stimulate such CTL in vivo, (II) are also  
 CC used: (i) as source of therapeutic antisense sequences that reduce  
 CC expression of (III); (ii) for recombinant production of (I); (iii)  
 CC particularly its fragments, as primers and probes in usual hybridisation  
 CC and amplification assays, for diagnosis, prognosis and monitoring of  
 CC tumours, or for measuring binding specificity of HLA molecules or CTL  
 CC clones; (iv) to identify related sequences; and (v) for generating  
 CC transgenic animals, e.g. for studying cancer and immune responses to it.  
 CC (I) are used to raise specific antibodies (Ab) and therapeutically. Ab  
 CC are used to diagnose tumours in immunoassays, also for delivering drugs,  
 CC toxins, imaging agents etc. to (I)-expressing cells. AAY49637 to AAY49670  
 CC represent exemplary tumour antigenic peptides given in the present  
 CC invention.

XX Sequence 15 AA;  
 SQ Query Match 100.0%; Score 83; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
 Db 1 DSYLQSDPDSFQD 15

**RESULT 5**  
 AAY01749 standard; peptide; 15 AA.  
 ID AAY01749;

XX DT 25-JUN-1999 (first entry)

DE Exemplary antigenic peptide derived from Tyrosinase.

XX XX MAGE-3; tumour associated gene; human leucocyte antigen Class II;  
 KW autologous CD4+ cell; MAGE-3 related disease; cancer; melanoma;  
 KW osteosarcoma; leukemia; carcinoma.

XX OS Homo sapiens.

XX PN WO9914326-A1.

XX XX Synthesis.

XX PD 25-MAR-1999.

XX PN 04-SEP-1998; 98WO-US018601.

XX PR 12-SEP-1997; 97US-00928615.

XX XX (LUDWIG) LUDWIG INST CANCER RES.

XX PA (UVT) UNIV VRIJE BRUSSEL.

XX PI Thielemans K, Heirman C, Cortahal J, Chaux P, Stroobant V;

PI Boon-Falleur T, Van Der Bruggen P, Luitjen R,

XX XX DR WPI; 1999-244031/20.

XX PT Isolated peptides that bind to human leucocyte antigen class II  
 PT molecules.

XX XX Disclosure; Page 29; 88pp; English.

XX The present sequence represents an exemplary tumour associated peptide  
 CC antigen. The specification describes a MAGE-3 tumour associated gene.

CC Peptides (AAV01749-21-25) that bind human leucocyte antigen (HLA) Class II  
 CC molecules can be derived from the MAGE-3 protein. These peptides and  
 CC autologous CD4+ cells that bind to a complex of MAGE-3 peptide and HLA  
 CC Class II are used to treat MAGE-3 related diseases, particularly cancers  
 CC (e.g. melanoma, osteosarcoma, leukemia and various forms of carcinoma).  
 CC The peptides are also used to produce specific antibodies. Detection of  
 CC the peptides, e.g. in binding assays, particularly with antibodies, is  
 CC used for diagnosis of such diseases.

XX Sequence 15 AA;

XX SQ Query Match 100.0%; Score 83; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15

Db 1 DSYLQSDPDSFQD 15

**RESULT 6**

AAY71516 standard; peptide; 15 AA.

XX AC AAY71516;

XX DT 12-OCT-2000 (first entry)

DE Human Tyrosinase peptide-6.

XX XX Tyrosinase; human; Tumour Rejection Antigen; TRA; tumour; cancer; HLA;

KW Human Leucocyte Antigen; MHC; Major Histocompatibility Complex; CTL;

KW cytolytic T-lymphocyte; immune response stimulator; prophylaxis; therapy;

KW diagnosis; TNF; tumour necrosis factor; vaccine; cytostatic.

XX OS Homo sapiens.

XX

PN WO200032759-A2.  
 XX  
 PD 08-JUN 2000.  
 XX  
 PF 26-NOV-1999; 99WO-IB002018.  
 XX  
 PR 27-NOV-1998; 98GB-00026143.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Huang L, Van Pei A, Brasseur F, De Plaen E, Boon T;  
 XX  
 DR WPI; 2000-412317/35.  
 XX  
 PT Novel polypeptides expressed in tumor cells useful for treating cancers  
 PT have an ability to complex with major histocompatibility complex  
 PT molecule and comprises a specific unbroken amino acid sequence.  
 XX  
 PS Disclosure; Page 19; 80pp; English.  
 XX  
 CC The patent discloses MAGE-A10 and MAGE-A8 polypeptide, nonapeptide and  
 CC decapeptide sequences, that function as tumour rejection antigens (TRAs).  
 CC These peptides are capable of forming a complex with major  
 CC histocompatibility complex (MHC) molecule type HLA-A2.1 (Human Leucocyte  
 CC Antigen), that are recognised by T-lymphocytes and elicit an immune  
 CC response from cytotoxic T-lymphocytes (CTL). They function as an immune  
 CC response stimulator. Tumour rejection antigens are useful in prophylaxis,  
 CC therapy and diagnosis of tumours and are effective in controlling or  
 preventing tumour growth. The present sequence is the human Tyrosinase  
 CC peptide-6, that corresponds to residues 448-462 of the tumour associated  
 Gene, tyrosinase encoding protein. It can be administered to induce or  
 enhance an immune response and is presented by HLA-DR4 complex. This  
 CC peptide can serve as a tumour rejection antigen (TRA) and in combination  
 CC with adjuvants, can produce vaccines useful for treating a variety of  
 CC tumours  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 83; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYSYLQDSPPDSFQD 15  
 Db 1 DYSYLQDSPPDSFQD 15  
 XX  
 RESULT 7  
 RAY0800 ID AAY90800 standard; peptide; 15 AA.  
 XX  
 AC AAY90800/  
 DT 25-AUG-2000 (first entry)  
 XX  
 DE Human leukocyte antigen DR4 peptide SEQ ID NO:29  
 XX  
 KW Human leukocyte antigen; HLA-B35; binding; recognition; lysis;  
 KW cytotoxic T cell; tyrosinase; immune response; diagnosis; identification;  
 KW human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200021551-A1.  
 XX  
 PD 20-APR-2000.  
 XX  
 PF 04-OCT-1999; 99WO-US023038.  
 XX  
 PR 09-OCT-1998; 98US-00169717.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Ooms A, De Giovanni G, Morel S, Van Den Eynde B, Boon-Falleur T;  
 XX  
 DR WPI; 2000-317842/27.  
 XX  
 PT Isolated peptides, sometimes derived from tyrosinase, which bind to HLA-B35 leading to recognition and lysis of the resulting complexes by cytotoxic T cells.  
 XX  
 PR Example 3; Page 9; 20pp; English.  
 XX  
 CC The present invention describes isolated peptides which bind to human  
 CC leukocyte antigen (HLA)-B35 molecules leading to recognition and lysis of  
 CC the resulting complexes by cytotoxic T cells. The isolated peptides are  
 CC sometimes derived from tyrosinase. Compositions comprising the peptides  
 CC of the invention can be used to generate immune responses, preferably in  
 CC humans, but also in non-human animals to generate immune components  
 CC which can then be used to treat humans or diagnostically.  
 CC Therapeutically, the peptides are useful in generation of cytolytic T  
 CC cells either in vitro or in vivo which specifically lyse pathogenic  
 CC cells. The peptides can also be used to identify HLA-B35 positive cells,  
 CC or to remove HLA-B35 positive cells from mixtures containing such cells.  
 CC Nucleic acid molecules encoding the peptides can be used inter alia as  
 CC probes to identify cells which are expressing tyrosinase. The present  
 CC sequence represents an HLA binding peptide used in the exemplification of  
 the present invention  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 83; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYSYLQDSPPDSFQD 15  
 Db 1 DYSYLQDSPPDSFQD 15  
 XX  
 RESULT 8  
 AAB23672 ID AAB23672 standard; peptide; 15 AA.  
 XX  
 AC AAB23672;  
 DT 05-JAN-2001 (first entry)  
 XX  
 DE Cytotoxic T lymphocyte (CTL) epitope SEQ ID NO:24.  
 XX  
 KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;  
 KW immune response; malaria; cytotoxic T cell;  
 KW cytosstatic; immunostimulant; cellular immune response inducer;  
 KW protozoacide; leukaemia; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO20049041-A1.  
 XX  
 PR 24-AUG-2000.  
 XX  
 PA (SUMITOMO ELECTRIC IND CO.  
 XX  
 PI Shinbara N, Udono H, Yui K;  
 XX  
 DR WPI; 2000-543748/49.  
 XX  
 PT Fused protein capable of inducing cellular immune response, useful as  
 PT active ingredient for drug compositions in preventing and/or treating  
 PT infectious diseases such as malaria or cancer.  
 XX  
 PS Claim 7; Page 57; 72pp; Japanese.

XX The present invention describes a fused protein (I) prepared from a  
 CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by  
 CC cytotoxic T cells and a protein containing the arspase domain of a heat  
 CC shock protein. Also described are: (1) a drug composition containing (I)  
 CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector  
 CC containing the DNA of (2); and (4) a transformant which can retain the  
 CC expression vector of (3). (I) has cytosatic, immunostimulant and  
 CC protozoacide activities, and can be used as a cellular immune response  
 CC inducer. The protein is useful as an active ingredient for drug  
 CC compositions in preventing and/or treating infectious diseases such as  
 CC malaria or cancer e.g. to provide systemic immunity against leukaemia.  
 CC The present sequence represents a specifically claimed CTL epitope for  
 CC use in a fused protein of the present invention

SQ Sequence 15 AA;

Query Match	100.0%	Score 83;	DB 3;	Length 15;
Best Local Similarity	100.0%	Pred. No. 1.7e-06;		
Matches	15;	Conservative 0;	Mismatches 0;	Indels 0;
Gaps	0;			

Qy	1 DYSYIQLQSDPSPFQD 15
Db	1 DYSYIQLQSDPSPFQD 15

RESULT 9

ID	AYA92296	standard; Peptide; 15 AA.
XX		
AC	AYA92296;	
XX		
DT	10-AUG-2000	(first entry)

DE	Tyrosinase antigenic peptide epitope (residues 448-462).
XX	
KW	Tyrosinase; antigen; epitope; cytotoxic T lymphocyte; CTL; complex;
KW	human leukocyte antigen; HLA.
XX	
OS	Homo sapiens.
NN	WO20002045-A2.
XX	
PD	13-APR-2000.
XX	
PF	15-SEP-1999; 99WO-IB001664.
XX	
PR	02-OCT-1998; 98US-00165863.
PR	09-APR-1999; 99US-00289350.
XX	
PA	(CHAU/) CHAUX P.
PA	(LUIT/) LUITEN R.
PA	(DEM0/) DEMOTTE N.
PA	(DUFF/) DUFFOUR M.
PA	(LURQ/) LURQUIN C.
PA	(TRAV/) TRAVERSARI C.
PA	(STRO/) STROOBANT V.
PA	(CORN/) CORNELIS G.R.
PA	(BOON/) BOON-FALLEUR T.
PA	(VBRU/) VAN DER BRUGGEN P.
PA	(SCHU/) SCHULTZ E.
PA	(WARN/) WARNER G.

XX	
PI	Chaux P, Luiten R, Demotte N, Duffour M, Lurquin C, Traversari C;
PI	Stroobant V, Cornelis GR, Boon-Falleur T, Van Der Bruggen P;
PI	Schultz E, Warnier G;
XX	
DR	2000-303739/26.

XX	
PI	Isolation of cytotoxic T-lymphocytes clones by successive steps of PT stimulation and testing of lymphocytes with antigen presenting cells PT which present antigens derived from different expression systems.
XX	

PS Disclosure; Page 22; 99pp; English.

XX A novel method of isolation of cytotoxic T-lymphocytes (CTL) clones  
 CC comprises successive steps of stimulation and testing of lymphocytes with  
 CC antigen presenting cells (APCs) which present antigens derived from  
 CC different expression systems. The CTL clones isolated recognize specific  
 CC antigenic peptides of proteins, preferably of the MAGE family. The APC is  
 CC autologous and each expression system is different from at least one of  
 CC the other expression systems, therefore isolating a cytotoxic T cell  
 CC clone specific for the protein. The method can also be used to identify  
 CC an antigenic peptide epitope. Isolated CTL clones specific for a  
 CC peptide/human leukocyte antigen (HLA) complex are claimed. The CTL cells  
 CC specific for the complexes, peptides or cells which present the complexes  
 CC on the cell surface are useful for treating pathological conditions  
 CC characterized by abnormal expression of the complexes

XX SQ Sequence 15 AA;

Query Match	100.0%;	Score 83;	DB 3;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 1.7e-06;		
Matches	15;	Conservative 0;	Mismatches 0;	Indels 0;
Gaps	0;			

Qy	1 DYSYIQLQSDPSPFQD 15
Db	1 DYSYIQLQSDPSPFQD 15

RESULT 10

ID	AYA56611	standard; peptide; 15 AA.
XX		
AC	AYA56611;	
XX		
DT	21-FEB-2000	(first entry)

XX	
DE	Tyrosinase gene MHC molecule HLA-DR4 peptide SEQ ID NO:27.
XX	
KW	HLA-A*0201; human leukocyte antigen; cytolytic T cell; CTL; tumour;
KW	Melan-A; Peripheral blood lymphocyte; PBL; immune complex; melanoma;
KW	MHC molecule; beta2-microglobulin; cytotoxic T lymphocyte; vaccine;
KW	immune response; cancer; tyrosinase; tumour rejection antigen;
KW	major histocompatibility complex.
XX	
OS	Synthetic.
OS	Homo Sapiens.
XX	
PN	W09950637-A2.
XX	
PD	07-OCT-1999.
XX	
PF	25-MAR-1999; 99WO-US006615.
XX	
PR	27-MAR-1998; 98US-00049850.
XX	
PA	(LUDW-) LUDWIG INST CANCER RES.
PA	(UYOX-) UNIV OXFORD.
XX	
PI	Romero P, Dunbar R, Valmori D, Ogg G, Cerronini J, Cerundolo V;
PI	Pittet M;
XX	
DR	2000-052636/04.

XX	
PT	New isolated complex of binding partners and immune complexes containing PT major histocompatibility molecules and peptide, used to isolate and detect PT cytotoxic T cells, particularly directed against cancer.
XX	
BS	Example 50: Page 64; 91pp; English.
XX	
CC	The present invention describes an isolated complex (A) comprising: (i)
CC	first and second binding partners (B1, B2); and (ii) several immune
CC	complexes (IC) containing a major histocompatibility complex (MHC)
CC	molecule (I), a beta2-microglobulin molecule (b2MG) and a peptide (III)
CC	that binds specifically to (I). (A) are used for analysis of cytolytic T

cells (CTL) for characterisation of an immune response to tumours or for monitoring vaccine trials. Particularly they are used to isolate or detect particular CTL (especially those in tumour-infiltrated lymph nodes), including visualisation of antigen-specific CTL and determination if the cells have been activated by *in vivo* exposure to antigen. Isolated precursor cells may be expanded *in vitro* to produce cells with high tumourcidal activity, for therapeutic or diagnostic use. A method from the present invention allows: (i) preselection of T cell clones for use in immunotherapy according to their homing molecules; and (ii) improves the lytic activity of T cells populations by inhibition of natural killer cell receptors. The present sequence represents a peptide used in the cell reclassification of the present invention.

AY84270-Y84303 represent peptides which are tumour associated antigens. They can be administered in conjunction with the tumour rejection antigen precursor of the invention to induce anti-tumour responses. The tumour rejection antigen precursor of the invention is encoded by an alternative open reading frame (ORF) of human macrophage colony stimulating gene. Peptides derived from the alternative ORF of macrophage-colony stimulating factor, when presented by an antigen presenting cell having a human leukocyte antigen (HLA) class I molecule, effectively induce the activation and proliferation of CD8<sup>+</sup> cytotoxic T lymphocytes. Polypeptide and nucleic acids derived from the alternate ORF of macrophage-colony stimulating factor are useful for enriching selectively a population of T lymphocytes with CD8<sup>+</sup> T lymphocytes. They are also useful for diagnosing a disorder characterized by expression of the polymerase chain reaction product.

Sequence 15 AA;					
			Query Match		
			Best Local Similarity		
			Matches 15; Conservative		
Qy	DB	CCC QQ	Score 83; 100 %; 100 %;	Pred. No. 1.7e 0;	Mismatches
			DYSYLDSDPDSFQD	15	
			DYSYLDSDPDSFQD	15	
			DYSYLDSDPDSFQD	15	

RESULT 12			
ID	AAV82975	ID	AAV82975 standard; peptide; 15 AA.
XX		XX	
XX		XX	AAV82975;
DT	19-JUN-2000	( first entry)	
XX			Tyrosinase tumour associated antigen
DE			
XX			Tumour; tumour associated antigen; probe; primer; HIAA, cytotoxic T-1 <sup>mlm</sup> ctrl; helper T-lymphocyte; MAGE; Bach beta catenin; tyrosinase; Melan-A;
KW			
KW			Homo sapiens.
XX			WO200006598-A1.
XX		XX	
PN		PN	10-FEB-2000.
XX		XX	
PD		PF	99WO-US016236.
XX		XX	
PF		PF	15-JUL-1999;
XX		XX	
PR		PR	29-JUL-1998;
XX		XX	
PA		PA	(LUDWIG) LUDWIG INST CANCER RES.

CCC identifying functional variants and mimetics  
 Sequence 15 AA:  
 XX  
 6Q Query Match 100.0%; Score 83; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0;  
 Caps 0;

administering autologous cytotoxic T-cells sufficient to ameliorate the disorder. Fragments of the HERV-AVL3-B coding sequence are useful as probes or amplification primers for determining the expression of HERV-AVL3-B genes, to express tumor associated polypeptides *in vivo* and *in vitro* and to prepare fragments of such polypeptides to synthesize antibodies. Antigenic peptides of HERV-AVL3-B can be useful for generating antibodies either alone or as fusion proteins, as components of immunoassay and for determining the binding specificity of HLA molecules and/or cytotoxic T lymphocyte (CTL) for HERV-AVL3-B proteins. Peptides derived from the HERV-AVL3-B coding sequence and which are presented by MHC molecules and recognised by CTL or helper T-lymphocytes can be combined with peptides from other tumour rejection antigens by preparation of hybrid polypeptides or pypptides to produce polytopes. This exemplary tumour associated peptide antigen corresponds to amino acid sequence 117-134 of the HERV-AVL3-B protein.

CC acids 44B-462 of the tyrosinase polypeptide. See also AAY82953-Y82986  
 XX Sequence 15 AA;  
 SQ Query Match 100.0%; Score 83; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 AC 1 DYSYIQLQSDPDSFQD 15  
 ID 1 DYSYIQLQSDPDSFQD 15  
 DB 1 DYSYIQLQSDPDSFQD 15

RESULT 13  
 AAB02618  
 ID AAB02618 standard; peptide; 15 AA.  
 XX AC AAB02618;  
 XX DT 18-AUG-2000 (first entry)  
 XX DE Tumour associated peptide antigen from Tyrosinase #7.  
 XX KW MAGE-A3; HLA class II; human leukocyte antigen; antibody; vaccine;  
 XX cancer; human; tumour; tumour associated gene product.  
 OS Homo sapiens.  
 XX PN WO200020581-A1.  
 XX PR 05-OCT-1999; 99WO-US021230.  
 XX PD 13-APR-2000.  
 XX PP 15-SEP-1999; 99WO-US021230.  
 XX PR 05-OCT-1999; 98US-00166448.  
 XX PA (LUDWIG INST CANCER RES.  
 PA (UVRV-) UNIV VRIJE BRUSSEL.  
 XX PI Chaux P, Stroobant V, Boon-Falleur T, Van Der Bruggen P;  
 PI Schultze ES, Van Snick J, Lethe B, Thielemans K, Cortahs J;  
 PI Heirman C;  
 XX DR WPI: 2000-317713/27.  
 XX PT New MAGE-A3 class II binding peptides, useful to diagnose and treat  
 tumors, are fragments of MAGE-A3 which bind to and are presented to T  
 lymphocytes by human leukocyte antigen class II molecules.  
 XX Disclosure: Page 33; 119pp; English.  
 CC The present invention relates to MAGE-A3 (tumour associated gene product)  
 CC human leukocyte antigen (HLA) class II-binding peptides (see AAB02566-  
 CC B02595, and AAB02633-B02637). These peptides are presented to T cells in  
 CC the context of HLA class II molecules. The peptides stimulate the  
 CC activity and proliferation of CD4+ T lymphocytes. The invention also  
 CC includes nucleotide sequences encoding MAGE-3A Peptides (see AAA37928 and  
 CC AAA37938-A37940). The peptides and nucleotide sequences can be used to  
 CC create antibodies against the MAGE-A3 peptides, the antibodies, Peptides  
 CC and nucleotide sequences can be used to create a vaccine. The peptides  
 CC are used to diagnose or treat a disorder characterized by expression of  
 CC MAGE-3, particularly cancer. The methods can also be used in the  
 CC diagnosis of disorders associated with MAGE-3 expression. Included in the  
 CC invention are other human tumour antigens (see AAB02596-B02637), and PCR  
 CC primers used in the course of the invention (see AAA37929-A37937 and  
 CC AAA37941-A37942)  
 XX SQ Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14  
 AAB08690  
 ID AAB08690 standard; peptide; 15 AA.  
 XX AC AAB08690;  
 XX DT 02-JAN-2001 (first entry)  
 XX DB Antigenic peptide from tumour rejection antigen tyrosinase.  
 XX KW Epha3; HLA class II-binding peptide; human leukocyte antigen; antigen;  
 XX CD4+ T lymphocyte; tumour associated gene; vaccine.  
 XX OS Homo sapiens.  
 XX PN WO2000050589-A1.  
 XX PR 31-AUG-2000.  
 XX PF 18-FEB-2000; 2000WO-US004326.  
 XX PR 22-FEB-1999; 99US-0121170P.  
 XX PR 08-OCT-1999; 99US-015B565P.  
 XX PA (LUDWIG INST CANCER RES.  
 XX PI Chiari R, Coulie P, Boon-Falleur T;  
 XX DR WPI: 2000-572089/53.  
 XX PT Novel tyrosine kinase receptor, EphA3 human leukocyte antigen (HLA) class  
 PT II binding peptide and nucleic acid encoding the receptor, useful for  
 PT diagnosing and treating conditions characterized by expression of EphA3  
 PT gene.  
 XX Disclosure: Page 35; 107pp; English.  
 XX CC AAB0868-B08704 represent antigenic peptides characteristic of tumours.  
 CC The peptide may be combined in vaccines with a human EphA3 HLA (human  
 CC leukocyte antigen) class II-binding peptide. EphA3 antigens, when  
 CC presented by an antigen presenting cell having a HLA class II molecule,  
 CC effectively induce activation and proliferation of CD4+ T lymphocytes.  
 CC EphA3 is a tumour associated gene. EphA3 HLA binding peptides are used  
 CC for selectively enriching a population of T lymphocytes. The peptides are  
 CC also used for diagnosing a disorder characterized by EphA3 or EphA3 HLA  
 CC binding peptide expression. The peptides are also used to treat a  
 CC disorder characterized by EphA3 expression. The EphA3 binding peptides  
 CC are useful in producing vaccines and antibody.

Query Match 100.0%; Score 83; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15  
 AAB02107  
 ID AAB02107 standard; peptide; 15 AA.  
 XX AC AAB02107;  
 XX DT 31-JUL-2001 (first entry)

DE Tyrosinase human leukocyte antigen-DR4-binding peptide #2.  
 XX Human; Cytostatic; immunogen; Tyrosinase; human leukocyte antigen; HLA;  
 KW CD8; cytotoxic T lymphocyte; cancer; carcinoma; melanoma; myeloma;  
 KW brain tumour; sarcoma; vaccine; gene therapy.  
 XX Homo sapiens.  
 OS WO200129220-A2.  
 XX PN 18-JUN-1999; 990US-00336091.  
 PD 26-APR-2001.  
 XX PR (LUDWIG) LUDWIG INST CANCER RES.  
 PF 19-OCT-2000; 2000WO-US028852.  
 XX PR 19-OCT-1999; 99US-0160374P.  
 PR 01-FEB-2000; 2000US-0179570P.  
 XX PA (LUDWIG) LUDWIG INST CANCER RES.  
 PI Heidecker L, Van Den Eynde B, Boon-Falleur T, Brasseur F;  
 DR Disclosure; Page 20; 69pp; English.  
 XX New antigenic Peptides derived from MAGE-A12 polypeptides, useful for  
 PT diagnosis and treatment of cancer, such as bladder, lung, breast, brain,  
 PT prostate and renal carcinomas.  
 XX PS Disclosure; Page 20; 69pp; English.  
 XX The patent discloses antigenic peptides derived from MAGE-A12 protein and  
 CC presented by human leukocyte antigens (HLAs). These antigenic peptides  
 CC when presented by an antigen presenting cell having a HLA class I  
 CC molecule, effectively induce the activation and proliferation of CD8+  
 cytotoxic T lymphocytes (CTLs). MAGE-A12 is useful for treating a subject  
 CC having a disorder characterised by expression of MAGE-A12. The protein  
 CC microarray comprising MAGE-A12 is useful for diagnosing a disorder,  
 CC especially cancer, by determining the binding of an antibody, T  
 CC lymphocytes or a HLA molecule isolated from the subject suspected of  
 CC having the disorder characterised by the expression of MAGE-A12. MAGE-A12  
 CC is useful for treating cancers, including bladder carcinomas, melanomas,  
 CC oesophageal, lung, head and neck, breast, colorectal carcinomas,  
 CC myelomas, brain tumours, sarcomas, prostate and renal carcinomas and to  
 CC produce antibodies. MAGE-A12 antibodies are useful for diagnosing  
 CC disorders characterised by expression of MAGE-A12 immunogenic  
 CC polypeptide. These MAGE-A12 peptides are used as vaccines. They are also  
 CC used in gene therapy. The present sequence is an antigenic peptide  
 CC derived from Tyrosinase. This peptide which is characteristic of tumours  
 CC is presented by HLA-DR4 MHC (major histocompatibility complex) and is  
 CC recognised by CTLs.  
 XX SQ Sequence 15 AA;

Query Match Score 83; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSYLQDSDPPSFQD 15  
 Db 1 DSYLQDSDPPSFQD 15

RESULT 16  
 AAB31350 ID AAB31350 standard; peptide; 15 AA.  
 XX SQ Sequence 15 AA;  
 AC XX AAB31350;  
 XX DT 20-APR-2001 (first entry)  
 XX DT 20-APR-2001 (first entry)  
 XX DE Exemplary antigen characteristic of tumours, derived from tyrosinase.  
 XX KW MAGE-A1; HLA; human leukocyte antigen; CD4+ T lymphocyte; cancer;  
 KW MAGE-A1 HLA class II-binding protein; vaccine.

XX Homo sapiens.  
 OS XX WO200078806-A1.  
 PN XX PR 14-JUN-2000; 2000WO-US016287.  
 PD XX PR 18-JUN-1999; 990US-00336091.  
 PA XX PA (LUDWIG) LUDWIG INST CANCER RES.  
 XX PI Van Snick J, Lethe B, Chaux P, Boon-Falleur T, Van Der Bruggen P;  
 DR XX WPI; 2001-102698/11.  
 XX PR Novel MAGE-A1 human leukocyte antigen class II peptides which bind to and  
 PR are presented to the class II molecules, useful for inducing immune  
 PR response and treating cancers characterized by expression of MAGE-A1.  
 XX PS Disclosure; Page 33; 78pp; English.  
 XX AAB31302-59 represent exemplary antigens which are characteristic of  
 CC tumours. They can be used to enhance the immune response of vaccines  
 CC comprising peptides derived from human MAGE-A1 HLA (human leukocyte  
 CC antigen) class II-binding protein. Peptides derived from the MAGE-A1 HLA  
 CC binding protein stimulate the activity and proliferation of CD4+ T  
 CC lymphocytes. The MAGE-A1 HLA binding protein is useful as a diagnostic  
 CC agent for diagnosing a disorder characterised by expression of MAGE-A1.  
 CC The protein is used for treating a disorder characterized by expression  
 CC of MAGE-A1 such as cancers e.g. melanoma, squamous cell carcinomas,  
 CC colorectal carcinomas, osteosarcomas, and lymphocytic leukemias. Peptides  
 CC derived from the MAGE-A1 HLA binding protein are useful in the production  
 CC of anti-tumour vaccines.  
 XX SQ Sequence 15 AA;  
 Query Match Score 100.0%; Score 83; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSYLQDSDPPSFQD 15  
 Db 1 DSYLQDSDPPSFQD 15

RESULT 17  
 AAE06837 ID AAE06837 standard; peptide; 15 AA.

XX SQ Sequence 15 AA;  
 AC XX AAE06837;  
 XX DT 16-OCT-2001 (first entry)  
 XX DE Human tyrosinase antigenic peptide #7.  
 XX KW MAGE antigenic peptide; Human leukocyte antigen; HLA-B35; HLA-B44;  
 KW tumour cell; immunostimulant; antigen presentation; cancer; melanoma;  
 KW CD8+ cytotoxic T lymphocyte; colorectal; prostate; gastric carcinoma;  
 KW myeloma; brain tumour; sarcoma; seminoma; ovarian tumour; cytostatic;  
 KW gene therapy; tumour resection antigen; TRA; human; tyrosinase; MHC;  
 KW major histocompatibility complex.

XX OS Homo sapiens.  
 XX PN WO200153833-A1.  
 XX PR 26-JUL-2001.  
 XX PR 19-JAN-2001; 2001WO-US002008.  
 XX PR 20-JAN-2000; 2000US-0177242P.

PR	25-OCT-2000;	2000US-0243212P.						
XX	(LUDWIG)	LUDWIG INST CANCER RES.						
PA								
XX								
PI	Luiten R,	Boon-Faillie T,	Van Der Bruggen P,	Stroobant V;				
PI	Demotte N,	Schultz E;						
XX	DR WPI:	2001-488724/53.						
PT	Functional variants and isolated mimetics of a MAGE-A1 HLA-B35 or HLA-B44 binding peptide, or of a MAGE-A3 HLA-B35 binding peptide, used in							
PT	diagnosis and treatment of a disorder characterized by expression of MAGE							
PT	-A1 or -A3.							
XX	PS Disclosure:	Page 28; 103pp; English.						
XX	The invention relates to functional variants and isolated mimetics of a MAGE-A1 human leukocyte antigen (HLA)-B35 or HLA-B44 binding peptide, or of a MAGE-A3 HLA-B35 binding peptide, identified by methods described in the specification. MAGE Genes encode tumour rejection antigens (TRAs) presented to T lymphocytes by HLA-B35 and HLA-B44 molecules. The MAGE antigenic peptide acts by binding to HLA molecules on tumour cells and stimulating recognition of these cells and thus signalling them to the immune system for destruction. The peptide when presented by HLA molecule induces the activation and stimulation of CD8+ cytotoxic T lymphocytes.							
CC	The MAGE antigenic peptide is used to treat and diagnose disorders characterized by expression of MAGE-A1 or -A3. Disorders include cancers e.g. melanomas, oesophageal, lung, head and neck, breast, colorectal, prostate, renal, bladder, hepatocellular, papillary thyroid and gastric carcinomas, myelomas, brain tumours, sarcomas, seminomas, and ovarian tumours. The present sequence is human tyrosinase tumour associated antigenic peptide presented by major histocompatibility complex (MHC) HLA -DR4. The antigenic peptide is used in combination with peptides of the invention for inducing an immune response							
XX	Sequence 15 AA;							
SQ	Query Match Best Local Similarity 100.0%; Score 83; DB 4; Length 15; Matches 15; Conservative 0; Mismatches 0; Gaps 0;							
Qy	1 DYSYIQLQSDPDPFSQD 15							
Db	1 DYSYIQLQSDPDPFSQD 15							
RESULT 18								
ABG7140								
ID	ABG7140 standard; peptide; 15 AA.							
XX								
AC	ABG7140;							
XX	DT 15-NOV-2002 (first entry)							
DE	Human tyrosinase class II HLA tumour-restricted antigen peptide #2.							
XX								
KW	Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen; lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia; kidney cancer; adenocarcinoma; breast cancer; cervical cancer; ovarian cancer; pancreatic cancer; tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA; cytosatic; human.							
XX	Homo sapiens.							
OS								
XX	WO200264057-A2.							
PN								
XX	22-AUG-2002.							
PD								
XX	15-FEB-2002; 2002WO-US005212.							
PF								
XX	18-MAY-2000; 2000US-00574749.							
PR								

XX (BAYU ) BAYLOR COLLEGE MEDICINE.  
XX  
PA  
XX  
PI  
XX  
DR WPI: 2002-627577/67.

XX Novel composition for treating a disease in an animal, comprises an immune effector cell and cell penetrating peptide associated with an antigen or antibody.

XX Disclosure: Page 22; 61pp; English.

XX The invention relates to a composition (I) comprising an immune effector cell and a cell penetrating peptide (CPP) associated with an antigen or antibody. Also included are (1) a vaccine comprising (I), CPP associated with an antigen, and a pharmaceutically acceptable carrier and (2) preparing a composition for a disease, by providing (I) and CPP associated with an antigen for disease, and introducing the antigen-associated CPP to (I), where antigen enters into the cell. The antigens are, for example, tumour antigen derived epitopes recognised by tumour infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I or II. The composition is useful for enhancing immunity in an animal to a disease, by administering a mature dendritic cell comprising CPP associated with an antigen to disease, to the animal, such that following the administration, animal is protected from disease, where the animal comprises both CD4+ and CD8+ T cells. It is also useful for treating a disease (e.g. cancer, tumour, melanoma, thymoma, sarcoma, lung cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma, breast cancer, prostate cancer, ovarian cancer and pancreatic cancer). The animal is further subjected to a cancer treatment including surgery, radiation, chemotherapy or gene therapy. The administration of (I), preferably dendritic cell is prior to, subsequent to or concurrent with, the cancer treatment. The present sequence is a tumour antigen derived epitope for inclusion in the composition of the invention

XX Sequence 15 AA;

XX

PR 12-NOV-1999; 99WO-US026795.  
 XX  
 PA (PYKE/) PYKETT M. J.  
 PA (ROSE/) ROSENZWEIG M.  
 PA (SCAD/) SCADDEN D. T.  
 PA (POZN/) POZNANSKY M. C.  
 XX  
 PI Pykett MJ, Rosenzweig M, Scadden DT, Poznansky MC;  
 XX DR WPI; 2003-605374/57.  
 XX Producing lymphoid tissue-specific cell in vivo, useful in  
 PT transplantation, implantation, autoimmune and/or infectious diseases by  
 PT introducing hematopoietic progenitor and lymphoreticular stromal cells  
 PT into a porous solid matrix.  
 XX Disclosure; SEQ ID NO 25; 34PP; English.  
 PS  
 CC The invention discloses a method for producing lymphoid tissue-specific  
 CC cell in vivo, comprising introducing haematopoietic progenitor cells and  
 CC lymphoreticular stromal cells into a porous, solid matrix having  
 CC interconnected pores of a pore size sufficient to permit the cells to  
 CC grow throughout the matrix, and co-culturing the haematopoietic  
 CC progenitor cells and lymphoreticular stromal cells. The methods are  
 CC useful in transplantation, implantation, autoimmune diseases and/or  
 CC infectious diseases. They are particularly useful for in vivo  
 CC maintenance, expansion and/or differentiation of haematopoietic  
 CC progenitor cells, for inducing T cell tolerance, for treating a subject  
 CC to enhance immune tolerance, for inducing T-cell reactivity, and for  
 CC identifying an agent suspected of affecting haematopoietic cell  
 CC development. The lymphoid tissue-specific cells are useful in laboratory  
 CC analysis and in therapeutics. The method provides rapid generation of a  
 CC large number of differentiated progeny. The sequence presented is a  
 CC cancer antigen which was used in the invention to expand haematopoietic  
 CC progenitor cells.  
 XX Sequence 15 AA;  
 SQ Query Match 100.0%; Score 83; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 15; Conservative 0; Mismatches -0; Indels 0; Gaps 0;  
 QY 1 DYSYIQLQDSDPDSFQD 15  
 Db 1 DYSYIQLQDSDPDSFQD 15  
 XX RESULT 20  
 AAU8418 AAU8418 standard; peptide; 30 AA.  
 XX AC AAU8418;  
 XX DT 08-MAY-2002 (first entry)  
 XX DE Human Tyros segment 30.  
 XX Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;  
 KW viral infection; human immunodeficiency virus; melanoma;  
 KW bacterial infection; Salmonella; Legionella; Giardia.  
 XX Homo sapiens.  
 XX PN WO200190197-A1.  
 XX XX 29-NOV-2001.  
 XX PR 25-MAY-2001; 2001WO-AU000622.  
 XX PR 26-MAY-2000; 2000AU-00007761.  
 XX PA (AUSU ) UNIV AUSTRALIAN NAT.

XX Thomson SA, Ramshaw IA;  
 XX PI WPI; 2002-147575/19.  
 XX DR N-PDB; ABK36738.  
 XX  
 PT New synthetic polypeptides having several different segments of at least  
 PT one parent polypeptide linked together differently compared to the  
 PT linkage in the parent polypeptide, for inducing immune response against a  
 PT pathogen or cancer.  
 XX Example 3; FIG 27; 364PP; English.  
 XX The invention relates to a new synthetic polypeptide (I) comprising  
 CC several different segments of at least one parent polypeptide linked  
 CC together in a different relationship relative to their linkage in the  
 CC parent polypeptide to impede, abrogate or otherwise alter at least one  
 CC function associated with the parent polypeptide and for inducing an  
 CC immune response against a pathogen or cancer. Also included are a  
 CC synthetic polynucleotide encoding and a computer system for designing the  
 CC synthetic polypeptides and polynucleotides  
 CC referred to as a Savine. The synthetic polypeptide is useful for  
 CC modulating immune responses preferentially directed against a pathogen or a  
 CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head  
 CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,  
 CC oesophagus, brain, testicle, uterus), as potentiating agents.  
 CC Compositions comprising the polypeptide may be used in the treatment or  
 CC prophylaxis against viral (such as infections caused by HIV (human  
 CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis  
 CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial  
 CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,  
 CC Salmonella, Streptococcus, Legionella and Mycobacterium or parasitic  
 CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,  
 CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is  
 CC a peptide derived from a parent protein used to construct a Savine of the  
 CC invention  
 XX SQ Sequence 30 AA;  
 Query Match 100.0%; Score 83; DB 5; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYSYIQLQDSDPDSFQD 15  
 Db 15 DYSYIQLQDSDPDSFQD 29  
 XX RESULT 21  
 AAW38167 AAW38167 standard; protein; 508 AA.  
 ID AAW38167;  
 AC AAW38167;  
 XX DT 13-MAR-1998 (first entry)  
 XX DE Mutant human tyrosinase (Pmel134A).  
 XX FN Key  
 PT Peptide  
 PT /label= sig\_Peptide  
 PT Peptide  
 PT /label= mat\_Peptide  
 PT  
 XX PN US5679511-A.  
 XX XX 21-OCT-1997.

XX 01-JUN-1992; 92US-00891942.  
 PF PR 06-OCT-1986; 86US-00915753.  
 XX PR 07-JUN-1989; 89US-00162847.  
 PA (GUTH-) GUTHRIE FOUND MEDICAL RES INC DONALD.  
 PA (INDV ) UNIV INDIANA FOUND.  
 XX PI Kwon BS;  
 XX DR WPI: 1997-525715/48.  
 DR N-PSDB; AAT93734.  
 XX PT Lambda mel 17-1 cDNA and Pmel17 protein - useful as melanin biosynthesis  
 probe.  
 XX PS Disclosure: Col 67-72; 67PP; English.  
 XX CC The present sequence is disclosed in the specification, which describes  
 CC the isolation of Pmel17, a protein encoded by cDNA isolated from lambda  
 CC mel 17-1 (ATCC 40264). The degree of melanisation in a human melanocyte  
 CC can be determined by subjecting human melanocyte RNA to a Northern blot  
 XX analysis, using the cDNA as a probe  
 Sequence 508 AA;

Query Match 100.0%; Score 83; DB 2; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYQLQDSDPDSFQD 15  
 Db 448 DYSYQLQDSDPDSFQD 462

RESULT 22  
 ID AAR56309 standard; protein; 529 AA.  
 XX AC AAR56309;  
 XX DT 25-MAR-2003 (revised)  
 DT 19-MAR-1995 (first entry)  
 XX DE Human tyrosinase acting as tumor rejection antigen precursor.  
 DE Tyrosinase; enzyme; tumor rejection antigen precursor; HLA;  
 KW human leukocyte antigen.  
 OS Homo sapiens.  
 XX PI Li L, Lishko VK;  
 FH Key Location/Qualifiers  
 FT Peptide 1..10  
 XX PN WO9414459-A1.  
 XX PD 07-JUL-1994.  
 XX PP 14-DEC-1993; 93WO-US012200.  
 XX PR 22-DEC-1992; 92US-00994928.  
 PR 28-APR-1993; 93US-00054714.  
 XX PR 23-JUN-1993; 93US-00081673.  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX PI Boon-Falleur T, Brichard V, Van Pel A, De Plae E, Coulie P;  
 PI Renauld J, Wolfel T, Lethe B;  
 XX DR WPI: 1994-234342/28  
 DR N-PSDB; AAQ66548.  
 XX

PT Method for the identification of HLA complexes - used for the detection  
 of abnormal cells.  
 XX Disclosure; Page 19; 31pp; English.

CC This normally occurring tyrosinase which may act as a tumor rejection  
 antigen precursor and be processed to form a peptide tumor rejection  
 antigen (AAR56310) which is presented on the surface of a cell, in  
 combination with HLA-A2, thereby stimulating lysis of cytotoxic T-  
 lymphocyte clones. (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 529 AA;

Query Match 100.0%; Score 83; DB 2; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYQLQDSDPDSFQD 15  
 Db 448 DYSYQLQDSDPDSFQD 462

RESULT 23  
 ID AAR63623 standard; protein; 529 AA.  
 XX AC AAR63623;  
 AC DYSYQLQDSDPDSFQD 15  
 XX DT 25-MAR-2003 (revised)  
 DT 21-JUN-1995 (first entry)  
 DE Human tyrosinase protein.  
 XX KW Human; tyrosinase; compound; hair; follicle; liposome; lipophilic;  
 KW lipophilic; stratum corneum; melanin; hair dye; Glycoprotein; alopecia;  
 KW chemotherapy; transforming growth factor; growth stimulant; aromatase;  
 KW cyclosporin A; macromolecule; polymer.  
 XX OS Homo sapiens.  
 XX PN WO9422468-A1.  
 XX PD 13-OCT-1994.  
 XX PF 01-APR-1994; 94WO-US003634.  
 XX PR 02-APR-1993; 93US-00041553.  
 PR 13-JAN-1994; 94US-00181471.  
 PA (ANTI-) ANTICANCER INC.  
 XX PI Li L, Lishko VK;  
 DR WPI; 1994-322816/41.  
 XX N-PSDB; AAQ72871.

PT Liposomes for delivering protein, nucleic acid etc. to hair follicles -  
 PR e.g. to restore hair colour, prevent hair loss during chemotherapy  
 PR stimulate hair growth etc.  
 XX

Claim 6; Page 67-70; 100pp; English.

PT The amino acid sequence of a human tyrosinase protein. This is an example  
 PR of a compound which can be delivered to hair follicles via a novel  
 CC liposome composition. The liposomes are comprised of a lipophilic or  
 CC lipophobic compound which will selectively target the hair follicle (via  
 CC the stratum corneum) without damaging or unwanted effects on cells  
 CC outside the follicle. Compounds e.g. tyrosinase (or the DNA encoding it),  
 CC melanin or hair dyes, can be delivered to the hair follicle to restore  
 CC hair colour or condition. Other compounds targeted at hair follicles can  
 CC include: p-glycoprotein (AQ072872) for treatment of chemotherapy-induced  
 CC alopecia; human transforming growth factor alpha (AAQ72873) for reversal  
 CC of wavy hair; hair growth stimulants (e.g. cyclosporin A or aromatase)

CC or antisense sequences. The methods allows compounds (e.g. macromolecules  
 CC or polymers), which would not normally reach the hair follicles, to be  
 delivered to these target areas. (Updated on 25-MAR-2003 to correct PN  
 CC field.)

SQ Sequence 529 AA;

Query Match 100.0%; Score 83; DB 2; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSYLQDSDPDSFQD 15  
 Db 448 DSYLQDSDPDSFQD 462

RESULT 24  
 AAW00184  
 ID AAW00184 standard; protein; 529 AA.  
 XX DT 18-OCT-1996 (first entry)  
 AC AAW00184;  
 XX PR Human tyrosinase.  
 XX KW Human; Tyrosinase; detection; primer; reverse transcription; amplify;  
 KW transcription region; detection.  
 XX OS Homo sapiens.  
 PN JP08140699-A.  
 XX PD 04-JUN-1996.  
 XX PF 22-NOV-1994; 94JP-00288041.  
 XX PR 22-NOV-1994; 94JP-00288041.  
 XX PA (POKK ) POLA CHEM IND INC.  
 XX DR WPI; 1996-316329/32.  
 DR N-PSDB; AT3331c.  
 XX PT Detection of tyrosinase mRNA - by amplification of tyrosinase mRNA allows  
 PT accurate detection of trace amounts of RNA.  
 XX Disclosure; Page 7-9; 10PP; Japanese.

CC This sequence represents human tyrosinase. The cDNA encoding this  
 CC sequence was detected by the method of the invention using the primers  
 CC given in AT33317-24. The method comprises synthesising tyrosinase cDNA  
 CC from a sample by reverse transcription and then amplifying the cDNA using  
 CC primers specific for, or complementary to, sequences within the  
 CC transcription region of the tyrosinase gene. Amplification using these  
 CC primers produces a competitive cDNA which can also be amplified. This  
 CC method can be used to specifically detect trace amounts of human  
 CC tyrosinase mRNA.

XX SQ Sequence 529 AA;

Query Match 100.0%; Score 83; DB 2; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSYLQDSDPDSFQD 15  
 Db 448 DSYLQDSDPDSFQD 462

RESULT 25  
 AAW00306  
 ID AAW00306 standard; protein; 529 AA.

XX AC AAW03306;  
 XX DT 22-OCT-1996 (first entry)  
 DE Tyrosinase melanoma antigen.  
 XX KW Melanoma; tyrosinase; immunogen; vaccine; cancer; immunootherapy;  
 KW transgenic animal.  
 XX OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Peptide  
 FT Peptide  
 FT Peptide  
 FT Peptide  
 XX WO9621734-A2.  
 XX PD 18-JUL-1996.  
 XX PF 11-JAN-1996; 96WO-US000473.  
 XX PR 10-JAN-1995; 95US-00370909.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX PI Robbins PF, Rosenberg SA;  
 XX DR WPI; 1996-342287/34.  
 XX DR N-PSDB; AAT35901.  
 XX PT Nucleic acid sequence encoding p15 melanoma antigen - and immunogenic  
 PT peptide(s) derived from it, useful for diagnosis, prevention or treatment  
 PT of melanoma.  
 XX Disclosure; Page 77-79; 98PP; English.  
 XX PS A DNA fragment (AAT35901) codes for tyrosinase (AAW03306), an enzyme  
 CC involved in melanin synthesis. The tyrosinase was recognised by HLA-A24  
 CC restricted tumour infiltrating lymphocytes from a melanoma patient.  
 CC Tyrosinase, or its immunogenic peptides (see also AAW03304-05), can be  
 CC used as a vaccine against melanoma, or to raise antibodies useful for the  
 CC diagnosis, assessment or prognosis of melanoma  
 XX SQ Sequence 529 AA;

Query Match 100.0%; Score 83; DB 2; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSYLQDSDPDSFQD 15  
 Db 448 DSYLQDSDPDSFQD 462

RESULT 26  
 AAW38166  
 ID AAW38166 Standard; protein; 529 AA.  
 XX AC AAW38166;  
 XX DT 13-MAR-1998 (first entry)  
 DE Normal human tyrosinase (Pmel134A).  
 XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human melanin;  
 KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;  
 KW tyrosinase; Pmel134A.  
 XX OS Homo sapiens.

FH	Key	Location/Qualifiers	XX	(UVI-) UNIV VIRGINIA PATENT FOUND.
FT	Peptide	1 .18 /label= sig_Peptide	XX	Slingluff CL, Hunt DF, Shabanowitz J, Cox AL, Engelhard VH;
FT	Peptide	19 .529 /label= mat_peptide	PI	Kittlesen D, Skipper J, Hendrikson RC;
XX			XX	
PN	US5679511-A.		DR	WPI; 1997-479982/44.
XX			XX	
PD	21-OCT-1997.	Melanoma-specific immunogens of pMEL-17 and tyrosinase - useful in	PR	Melanoma-specific immunogens of pMEL-17 and tyrosinase - useful in
XX	01-JUN-1992;	vaccination for producing melanoma-specific cytotoxic T lymphocytes.	PT	vaccination for producing melanoma-specific cytotoxic T lymphocytes.
PP	92US-00891942.	XX	XX	
XX		Disclosure; Fig 10; 106pp; English.	PS	Disclosure; Fig 10; 106pp; English.
PR	06-OCT-1986;	A novel melanoma specific immunogen comprises at least 1 melanoma	XX	A novel melanoma specific immunogen comprises at least 1 melanoma
PR	B6US-000915753.	specific cytotoxic T lymphocyte (CTL) epitope, where at least 1 of the	CC	specific cytotoxic T lymphocyte (CTL) epitope, where at least 1 of the
XX	07-JUN-1989;	CC epitopes is substantially homologous to a human leukocyte antigen-A1 (HLA	CC	CC epitopes is substantially homologous to a human leukocyte antigen-A1 (HLA
PA	(GUTH-) GUTHRIE FOUND MEDICAL RES INC DONALD.	-A1) and HLA-A3 restricted epitope of a melanoma antigen, either pMEL-17	CC	-A1) and HLA-A3 restricted epitope of a melanoma antigen, either pMEL-17
PA	(INDV ) UNIV INDIANA FOUND.	or tyrosinase, i.e. the present sequence. The immunogen can be used in	CC	or tyrosinase, i.e. the present sequence. The immunogen can be used in
XX		CC vaccines for protection against melanoma in mammals.	CC	CC vaccines for protection against melanoma in mammals.
PI	Kwon BS;	XX	XX	
XX	WPI; 1997-525715/48.	Sequence 529 AA;	SQ	Sequence 529 AA;
DR	N-PSDB; AAT95733.	Query Match 100.0%; Score 83; DB 2; Length 529;	Qy	Query Match 100.0%; Score 83; DB 2; Length 529;
PT	Lambda mel 17-1 cDNA and Fmell17 protein - useful as melanin biosynthesis	Best Local Similarity 100.0%; Pred. No. 9.3e-05;	Db	Best Local Similarity 100.0%; Pred. No. 9.3e-05;
PT	probe.	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PS	Disclosure; Col 59-64; 67pp; English.	Db 448 DYSYLOQSDPDSFQD 462	Db	448 DYSYLOQSDPDSFQD 462
XX		RESULT 28		
CC	The present sequence is disclosed in the specification, which describes	ID AAW71234 standard; protein; 529 AA.	XX	
CC	the isolation of Fmell17, a protein encoded by cDNA isolated from Lambda	XX	AAW71234;	
CC	mel 17-1 (ATCC 40264). The degree of melanisation in a human melanocyte	XX	AC 448;	
CC	can be determined by subjecting human melanocyte RNA to a Northern blot	XX	DT 16-NOV-1998 (first entry)	
CC	analysis, using the cDNA as a probe.	XX	DE Tyrosinase.	
XX	Sequence 529 AA;	XX	KW Tyrosinase; tyrosinase cytotoxic lymphocyte response;	
XX	Query Match 100.0%; Score 83; DB 2; Length 529;	XX	KW cytotoxic T lymphocyte; cysteine-depleted; melanoma.	
XX	Best Local Similarity 100.0%; Pred. No. 9.3e-05;	OS Synthetic.	XX	
XX	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	OS Synthetic.	
Qy	1 DYSYLOQSDPDSFQD 15	RESULT 27	XX	
Db	448 DYSYLOQSDPDSFQD 462	ID AAW36519	PN WO9831810-A2.	
XX	DT 08-APR-1998 (first entry)	ID AAW36519 standard; protein; 529 AA.	XX	
DE	Tyrosinase containing human leukocyte antigen-A1 epitope.	XX	PD 06-AUG-1998.	
XX	Melanoma; immunogen; cytotoxic T lymphocyte; CTL;	XX	PP 29-JAN-1998;	
KW	human leukocyte antigen-A1; HLA-A1; human leukocyte antigen-A3; HLA-A3;	XX	PP 30-JAN-1997;	
KW	epitope; pMEL-17; tyrosinase; vaccine; protection.	XX	PR 97US-0037781P.	
OS	Homo sapiens.	XX	PR (UVI-) UNIV VIRGINIA PATENT FOUND.	
FH	Key	Location/Qualifiers	PI Slingluff CL, Hunt DF, Engelhard VH, Kittlesen D;	
FT	Region	243 . 251	XX	
FT		/note= "human leukocyte antigen-A1 epitope"	DR WPI; 1998-437388/37.	
XX			XX	
PN	WO9734613-A1.	PS Disclosure; Fig 5; 93pp; English.	XX	
XX	25-SEP-1997.	CC The tyrosinase is used as a template for tyrosinase cytotoxic lymphocyte	CC	
PD		CC response peptides. These peptides are examples of cytotoxic T lymphocyte	CC	
XX		CC (CTL) epitopes which are cysteine-depleted mutants of a native disease-	CC	
XX		CC specific CTL epitope. The cysteine-depleted CTL epitopes elicit a	CC	
PP	17-MAR-1997;	CC stronger or more specific CTL response than the native epitope. The	CC	
XX	97WO-US004958.	CC tyrosinase epitopes are melanoma-specific and can be used in a disease-	CC	
PR	19-MAR-1996;	CC specific immunogen to protect a mammal against melanoma. The peptides may	CC	
PR	96US-0027627P.	CC also be used to screen a sample for the presence of an antigen with the	CC	

CC same epitope, or with a different cross-reactive epitope  
 XX Sequence 529 AA;

Query Match 100.0%; Score 83; DB 2; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OS Homo sapiens.

Qy 1 DSYLQDSDPDSFQD 15  
 Db 448 DSYLQDSDPDSFQD 462

RESULT 29  
 AAB51344 ID AAB51344 standard; protein; 529 AA.  
 XX AC AAB51344;  
 XX DT 09-APR-2001 (first entry)  
 XX DE Human tyrosinase protein sequence SBQ ID NO:4.  
 XX Human; tyrosinase; anti-gray hair agent; hair colour; hair follicle.  
 XX OS Homo sapiens.  
 XX PN JPP2000300298-A.  
 XX PD 31-OCT-2000.  
 XX PF 23-APR-1999; 99JP-00117006.  
 XX PR 23-APR-1999; 99JP-00117006.  
 XX (SHIS ) SHISEIDO CO LTD.  
 PA WPI; 2001-141361/15.  
 DR N-PSDB; AAF26897.  
 PT Screening the effect of an anti-gray hair agent.  
 XX Disclosure; Page 7-8; 11pp; Japanese.  
 PS Sequence 529 AA;

XX The present invention describes a method for separating the mRNA encoding tyrosinase in a hair follicle for the assumption of hair colour and for screening an anti-gray hair agent. The method is useful for screening an anti-gray hair agent and judging the effect of it. The present sequence represents human tyrosinase which is given in the exemplification of the present invention  
 XX Sequence 529 AA;

Query Match 100.0%; Score 83; DB 4; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OS Homo sapiens.

Qy 1 DSYLQDSDPDSFQD 15  
 Db 448 DSYLQDSDPDSFQD 462

RESULT 30  
 ABB86039 ID ABB86039 standard; protein; 529 AA.  
 XX AC ABB86039;  
 XX DT 16-JUL-2001 (first entry)  
 XX DE Human tyrosinase protein.  
 XX Listeria; expression vector; tumor-associated antigen; Trp 1; Trp 2;

KW MelanA/MART-1; cytostatic; attenuated; immunotherapy; malignant melanoma;  
 KW pigmented tumor; malignant schwannoma; vaccination; tyrosinase;  
 KW antigen-presenting cell.  
 XX OS Homo sapiens.  
 XX PN WO200127295-A1.  
 XX PD 19-APR-2001.  
 XX PP 13-OCT-2000; 2000WO-DE003629.  
 XX PR 14-OCT-1999; 99DE-01049594.  
 XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 XX PI Schadendorf D, Paschen A, Chakraborty T, Domann E;  
 XX DR WPI; 2001-282041/29.  
 XX DR N-PSDB; AAF88041.  
 XX Listeria expression vector for immunotherapy, particularly of malignant  
 PT melanoma, comprises a DNA sequence encoding tumor-associated antigens.  
 XX Disclosure; Fig 1; 41pp; German.  
 XX This invention describes a novel Listeria expression vector (A) for  
 CC immunotherapy which comprises a promoter (P), functional in Listeria,  
 CC operably linked to a DNA sequence (I) encoding one of the tumor-  
 CC associated antigens (II) human tyrosinase, Trp 1 or 2, or MelanA/MART-1.  
 CC The products of the invention have cytostatic activity. Recombinant  
 CC attenuated Listeria containing (A) are useful for immunotherapy  
 CC (prophylactic, adjuvant or therapeutic), specifically of malignant  
 CC melanoma (but also other pigmented tumors such as malignant schwannoma),  
 CC particularly as a replacement for radiotherapy. Using attenuated Listeria  
 CC as carrier for (A) provides a simple way of vaccination, since antigen-  
 CC presenting cells acquire tumor-associated antigens by natural infection,  
 CC eliminating the need for labor-intensive ex vivo modification of  
 CC autologous cells. This sequence represents the human tyrosinase protein  
 CC described in the method of the invention  
 XX SQ Sequence 529 AA;  
 XX Query Match 100.0%; Score 83; DB 4; Length 529;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX OS Homo sapiens.

Qy 1 DSYLQDSDPDSFQD 15  
 Db 448 DSYLQDSDPDSFQD 462

RESULT 31  
 AAU84806 ID AAU84806 standard; protein; 529 AA.  
 XX AC AAU84806;  
 XX DT 08-MAY-2002 (first entry)  
 XX DB Human Tyros consensus sequence.  
 XX SQ Sequence 529 AA;  
 XX Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;  
 KW viral infection; human immunodeficiency virus; melanoma;  
 KW bacterial infection; Salmonella; Legionella; Giardia.  
 KW Trypanosoma; Toxoplasma;  
 XX OS Homo sapiens.  
 XX PN WO200190197-A1.  
 XX DR 29-NOV-2001.

PF 25-MAY-2001; 2001WO-AU000622.  
 XX  
 PR 26-MAY-2000; 2000AU-00007761.  
 XX  
 PA (AUSU ) UNIV AUSTRALIAN NAT.  
 XX  
 Thomson SA, Ramshaw IA;  
 XX  
 PT WPI; 2002-147575/19.  
 XX  
 PT New synthetic polypeptides having several different segments of at least one parent polypeptide linked together differently compared to the PT linkage in the parent polypeptide, for inducing immune response against a pathogen or cancer.  
 XX  
 PS Example 3; Fig 27; 364pp; English.

XX The invention relates to a new synthetic polypeptide (I) comprising several different segments of at least one parent polypeptide linked together in a different relationship relative to their linkage in the parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide and for inducing an immune response against a pathogen or cancer. Also included are a synthetic polynucleotide encoding and a computer system for designing the synthetic polypeptides and polynucleotides referred to as Savine. The synthetic polypeptide is useful for modulating immune responses preferably directed against a pathogen or a cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone liver, oesophagus, brain, testicle, uterus), as potentiating agents. Compositions comprising the polypeptide may be used in the treatment or prophylaxis against viral (such as infections caused by HIV (human immunodeficiency virus), hepatitis, influenza, Japanese encephalitis virus, Epstein-Barr virus and respiratory syncytial virus), bacterial (e.g., infections caused by Neisseria, Meningococcal, Haemophilus, Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic (e.g., infections caused by Plasmodium, Schistosoma, Leishmania, Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is a consensus sequence for a parent protein used to design a savine of the invention

XX Sequence 529 AA;  
 SQ Score 83; DB 5; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQDSDPDSFQD 15  
 Db 448 DYSYLQDSDPDSFQD 462

RESULT 32  
 AAU11544 Human Melanoma tumour associated antigen tyrosinase.  
 ID AAU11544 standard; protein; 529 AA.  
 XX  
 AC AAU11544;

DT 12-MAR-2002 (first entry)  
 XX Human Melanoma tumour associated antigen tyrosinase.

DE Human Melanoma tumour associated antigen tyrosinase.

XX Human Melanoma tumour associated antigen tyrosinase.

KW Human; melanoma tumour associated antigen; human leukocyte antigen; major histocompatibility complex; MHC; HLA-A2; vaccine; cancer; HIV; KW human immunodeficiency virus infection; cytostatic; virucide; KW housekeeping epitope; adoptive immunotherapy; neoplastic disease; KW viral disease; hepatitis virus; papilloma virus; tumour; leukaemia; KW lymphoma; breast cancer; prostate cancer; lung cancer; tyrosinase; KW parasitic infection; Chlamydia; Trypanosoma; Toxoplasma.  
 XX OS Homo sapiens.  
 XX  
 PN WO200182963-A2.

XX  
 PF 08-NOV-2001.  
 XX  
 PD 27-APR-2001; 2001WO-US013806.  
 XX  
 PR 2B-APR-2000; 2000US-00560455.  
 PR 2B-APR-2000; 2000US-00561074.  
 PR 2B-APR-2000; 2000US-00561571.  
 PR 2B-APR-2000; 2000US-00561572.  
 XX  
 PA (CTLI) CTL IMMUNOTHERAPIES CORP.  
 XX  
 PT Simard JJL, Diamond DC, Lei X;  
 XI  
 DR WPT; 2002-065492/09.  
 XX  
 PS Novel vaccine useful for treating neoplastic and viral diseases, PR comprises a first housekeeping epitope derived from a first antigen associated with a first target cell.  
 XX  
 Example 24; Fig 18; 131pp; English.  
 XX  
 CC The invention relates to a vaccine comprising a first housekeeping epitope derived from a first antigen associated with a first target cell. Also included are an isolated T cell receptor specific for a major histocompatibility complex (MHC)-peptide complex comprising a first housekeeping epitope which is derived from a first antigen associated with a first target cell, selecting an epitope (or peptide sequence) from a population of peptide fragments of an antigen associated with a target in a host, where the fragments have a known or predicted affinity for a MHC receptor peptide binding cleft of the host, where the epitope selected corresponds to a product of proteolytic cleavage of the antigen in a cell of the host and a nucleic acid construct comprising a first coding region, where the first coding region comprises a first sequence encoding at least a first polypeptide, where the first polypeptide comprises a first housekeeping epitope derived from a first antigen associated with a first target cell; The epitopes, peptides, vaccines and nucleic acids are useful in the manufacture of a medicament for use in adoptive immunotherapy and for prevention and treatment of neoplastic and viral diseases (e.g., human immunodeficiency virus, HIV infection, hepatitis virus and papilloma virus), cancers (e.g., tumours, leukaemia, lymphoma, breast cancer, prostate cancer and lung cancer), infection of cells by intracellular parasites (e.g., Chlamydia, Trypanosoma and Toxoplasma) and many other examples given in the specification. The invention permits the vaccine designer to ignore peptides that, despite predicted high binding affinity for MHC, will never be useful because they cannot be presented by target cells. The invention provides a major advance in vaccine design, one that combines the power of antigen sequence analysis with the fundamental realities of immunology. The invention allows for the simple and effective selection of meaningful epitopes for creation of MHC class I or Class II vaccines using any polypeptide sequence corresponding to a desired target. The present sequence is an HLA-A2.1 (human leukocyte antigen) presenting target cell protein from which epitopes of the invention may be derived,  
 XX Sequence 529 AA;

SQ Query Match 100.0%; Score 83; DB 5; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQDSDPDSFQD 15  
 Db 448 DYSYLQDSDPDSFQD 462

RESULT 33  
 ABP74129 Human Melanoma tumour associated antigen tyrosinase.  
 ID ABP74129 standard; protein; 529 AA.  
 XX  
 AC AC  
 XX  
 PN ABP74129

1 DYSYLQDSDPDSFQD 15  
 448 DYSYLQDSDPDSFQD 462

RESULT 33  
 ABP74129 Human Melanoma tumour associated antigen tyrosinase.  
 ID ABP74129 standard; protein; 529 AA.  
 XX  
 AC AC  
 XX

DT 03-FEB-2003 (first entry)  
 XX Human tyrosinase protein SEQ ID NO:2.

XX Human; epitope; vaccine; immunotherapy; cytostatic; immunogenicity;  
 KW T cell; enzyme.

XX Homo sapiens.

XX PN WO200281646-A2.

XX PD 17-OCT-2002.

XX PR 04-APR-2002; 2002WO-US011101.

XX PA (CTLI-) CTL IMMUNOTHERAPIES CORP.

XX PI Simard JJL, Diamond DC, Liu L, Xie Z;

XX DR WPI; 2003-067518/06.

XX DR N-PSDB; ABQ83843.

XX PS Claim 1; Page 145; 352pp; English.

XX The present invention describes an isolated epitope (1) and an epitope cluster. Also described is a vaccine or immunotherapeutic composition comprising (1). (1) has cytostatic activity.

XX treating an animal, by administering to an animal the vaccine or immunotherapy composition. (1) is also useful for evaluating the immunogenicity of a vaccine or immunotherapeutic composition, by administering (1) to an HLA-transgenic animal and evaluating immunogenicity based on a characteristic of the animal, or by in vitro primary stimulation of a T cell and evaluating immunogenicity. (1) is useful for determining specific T cell frequency, by contacting T cell with a MHC-peptide complex, and further comprises ELISPOT analysis, limiting dilution analysis, flow cytometry, *in situ* hybridisation and/or polymerase chain reaction (PCR). ABQ83843 to ABQ83858 and ABP74128 to ABP74173 represent sequences used in the exemplification of the present invention.

XX Sequence 529 AA;

XX Query Match 100.0%; Score 83; DB 6; Length 529;

XX Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

XX Qy 1 DYSYKQDSDPDSDQD 15  
 Db 448 DYSYKQDSDPDSDQD 462

XX Query Match 100.0%; Score 83; DB 6; Length 529;

XX Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

XX Qy 1 DYSYKQDSDPDSDQD 15  
 Db 448 DYSYKQDSDPDSDQD 462

XX Query Match 100.0%; Score 83; DB 6; Length 529;

XX Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

XX Qy 1 DYSYKQDSDPDSDQD 15  
 Db 448 DYSYKQDSDPDSDQD 462

XX Query Match 100.0%; Score 83; DB 6; Length 529;

XX Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

XX Qy 1 DYSYKQDSDPDSDQD 15  
 Db 448 DYSYKQDSDPDSDQD 462

XX Query Match 100.0%; Score 83; DB 6; Length 529;

XX Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

XX Qy 1 DYSYKQDSDPDSDQD 15  
 Db 448 DYSYKQDSDPDSDQD 462

XX Query Match 100.0%; Score 83; DB 6; Length 529;

XX Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

XX Qy 1 DYSYKQDSDPDSDQD 15  
 Db 448 DYSYKQDSDPDSDQD 462

XX Query Match 100.0%; Score 83; DB 6; Length 529;

XX Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

XX Qy 1 DYSYKQDSDPDSDQD 15  
 Db 448 DYSYKQDSDPDSDQD 462

XX Query Match 100.0%; Score 83; DB 6; Length 529;

XX Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

XX Qy 1 DYSYKQDSDPDSDQD 15  
 Db 448 DYSYKQDSDPDSDQD 462

XX Query Match 100.0%; Score 83; DB 6; Length 529;

XX Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

XX Qy 1 DYSYKQDSDPDSDQD 15  
 Db 448 DYSYKQDSDPDSDQD 462

XX Query Match 100.0%; Score 83; DB 6; Length 529;

XX Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

XX Qy 1 DYSYKQDSDPDSDQD 15  
 Db 448 DYSYKQDSDPDSDQD 462

XX Query Match 100.0%; Score 83; DB 6; Length 529;

XX Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

XX Qy 1 DYSYKQDSDPDSDQD 15  
 Db 448 DYSYKQDSDPDSDQD 462

XX Query Match 100.0%; Score 83; DB 6; Length 529;

XX Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

XX Qy 1 DYSYKQDSDPDSDQD 15  
 Db 448 DYSYKQDSDPDSDQD 462

XX Query Match 100.0%; Score 83; DB 6; Length 529;

XX Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

XX Qy 1 DYSYKQDSDPDSDQD 15  
 Db 448 DYSYKQDSDPDSDQD 462

XX Query Match 100.0%; Score 83; DB 6; Length 529;

XX Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

XX Qy 1 DYSYKQDSDPDSDQD 15  
 Db 448 DYSYKQDSDPDSDQD 462

XX Query Match 100.0%; Score 83; DB 6; Length 529;

XX Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

XX Qy 1 DYSYKQDSDPDSDQD 15  
 Db 448 DYSYKQDSDPDSDQD 462

XX Query Match 100.0%; Score 83; DB 6; Length 529;

XX Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

XX Qy 1 DYSYKQDSDPDSDQD 15  
 Db 448 DYSYKQDSDPDSDQD 462

XX Query Match 100.0%; Score 83; DB 6; Length 529;

XX Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

XX Qy 1 DYSYKQDSDPDSDQD 15  
 Db 448 DYSYKQDSDPDSDQD 462

XX Query Match 100.0%; Score 83; DB 6; Length 529;

XX Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

XX Qy 1 DYSYKQDSDPDSDQD 15  
 Db 448 DYSYKQDSDPDSDQD 462

XX Query Match 100.0%; Score 83; DB 6; Length 529;

XX Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

XX Qy 1 DYSYKQDSDPDSDQD 15  
 Db 448 DYSYKQDSDPDSDQD 462

XX Query Match 100.0%; Score 83; DB 6; Length 529;

XX Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

XX Qy 1 DYSYKQDSDPDSDQD 15  
 Db 448 DYSYKQDSDPDSDQD 462

XX Query Match 100.0%; Score 83; DB 6; Length 529;

XX Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

XX Qy 1 DYSYKQDSDPDSDQD 15  
 Db 448 DYSYKQDSDPDSDQD 462

XX Query Match 100.0%; Score 83; DB 6; Length 529;

XX Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

XX Qy 1 DYSYKQDSDPDSDQD 15  
 Db 448 DYSYKQDSDPDSDQD 462

XX Query Match 100.0%; Score 83; DB 6; Length 529;

XX Best Local Similarity 100.0%; Pred. No. 9.3e-05; Indels 0; Gaps 0;

XX Qy 1 DYSYKQDSDPDSDQD 15  
 Db 448 DYSYKQDSDPDSDQD 462

KW immunisation.  
 OS Unidentified.  
 XX WO2003008537-A2.  
 XX PN 30-JAN-2003.  
 XX PD 29-MAR-2002; 2002WO-US010189.  
 PP PR 06-APR-2001; 2001US-028211P.  
 PR 07-NOV-2001; 2001US-033701P.  
 PR 07-MAR-2002; 2002US-0353210P.  
 XX PA (CTLI-) CTL IMMUNOTHERAPIES CORP.  
 XX PI Simard JJL, Diamond DC, Liu L, Xie Z;  
 XX SEQ ID NO 2; 239pp; English.  
 XX PT Epitope having high affinity for major histocompatibility complex class I useful for treating an animal, evaluating immunogenicity of a vaccine or therapeutic composition and for diagnosing a disease.  
 XX PCT 2003-248010/24.  
 XX Claim 1; SEQ ID NO 2; 239pp; English.  
 CC The invention relates to an isolated epitope polypeptide that has high affinity for major histocompatibility complex (MHC) class I, and an epitope cluster comprising the polypeptide. Also disclosed is a vaccine or immunotherapeutic composition containing an epitope of the invention. Compositions of the invention may be used in the treatment of cancer. The method can be combined with a radiation therapy, chemotherapy, biochemotherapy or surgery. The composition is also useful for evaluating immunogenicity of a vaccine or immunotherapeutic compound. Multimeric MHC -peptide complexes of the invention are useful for determining specific T cell frequency. This method is useful for evaluating immunological response, by performing the method prior to and subsequent to an immunisation step. Compositions of the invention are useful for diagnosing a disease. The current sequence represents an epitope of the invention with high affinity for MHC class I.  
 XX Sequence 529 AA;  
 CC Query Match 100.0%; Score 83; DB 7; Length 529;  
 CC Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 CC Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC QY 1 DYSYLQDSDPDSFQD 15  
 CC Db 448 DYSYLQDSDPDSFQD 462  
 CC Sequence encoded by human tyrosinase BBTY-1 cDNA.  
 XX Tyrosinase; enzyme; melanosomes; melanin; melanocyte.  
 XX Homo sapiens.  
 OS Key Qualifiers  
 XX Location/Qualifiers 1..19  
 FT /label= signal  
 FT Protein 20..531  
 XX WO9012869-A.

XX 01-NOV-1990.  
 XX 26-APR-1989; 89US-00343960.  
 PF XX 25-APR-1989; 89US-00343960.  
 PR XX (SLOK ) SLOAN KETTERING INST CANCER.  
 PA XX Non-melanocyte eukaryotic cell - expressing biologically active human tyrosinase and used in studying tyrosine synthesis.  
 PT XX Disclosure; Fig 1; 49pp; English.  
 XX A cDNA library was constructed from mRNA prepared from the human melanotic melanoma cell line SK-MEL-19. For screening, a 50 base probe was used (see AAC06551). The cDNA clone BBTY-1 was isolated, sequenced (see AAC06552) and analysed for tyrosinase activity. (Updated on 25-MAR-2003 to correct PA field.)  
 SQ Sequence 531 AA;  
 CC Query Match 100.0%; Score 83; DB 2; Length 531;  
 CC Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 CC Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC QY 1 DYSYLQDSDPDSFQD 15  
 CC Db 450 DYSYLQDSDPDSFQD 464  
 RESULT 37  
 AR79493 standard; protein; 531 AA.  
 AC XX AR79493;  
 AC DT 10-FEB-1996 (first entry)  
 AC XX Human tyrosinase acting as a tumor rejection antigen precursor.  
 AC XX DB Human tyrosinase standard; protein; 531 AA.  
 AC XX QY 1 DYSYLQDSDPDSFQD 15  
 AC Db 450 DYSYLQDSDPDSFQD 464  
 RESULT 38  
 AR07071 standard; protein; 531 AA.  
 ID XX AR07071 (revised)  
 AC XX AR07071;  
 AC DT 09-MAR-1992 (first entry)  
 AC XX Sequence encoded by human tyrosinase BBTY-1 cDNA.  
 AC XX Tyrosinase; enzyme; melanosomes; melanin; melanocyte.  
 AC XX Homo sapiens.  
 OS Key Peptide  
 XX Location/Qualifiers 1..19  
 FT /label= signal  
 FT Protein 20..531  
 XX WO95-311542/40.  
 DR N-PSDB; AAC01009  
 XX Cytolytic T cell specificity for MHC complexes - used to treat individual(s) with cellular abnormality, e.g. tumour(s).  
 PR XX Disclosure; Page 30-33; 57pp; English.  
 PS XX Human tyrosinase may act as a tumor rejection antigen precursor (TRAP) and be processed to form a peptide tumor rejection antigen which is

CC presented on the surface of the cell, in combination with HLA-A2, thereby  
 CC stimulating lysis by cytotoxic T-lymphocyte clones  
 XX Sequence 531 AA;  
 SQ Query Match 100.0%; Score 83; DB 2; Length 531;  
 CC Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 CC Matches 15; Conservative 0; Mismatches 0; Indels 0;  
 CC Gaps 0;

QY 1 DYSYLQDSDPDSFQD 15  
 DB 450 DYSYLQDSDPDSFQD 464

## RESULT 38

AAW22083 standard; Protein; 531 AA.

ID AAW22083

XX AC AAW22083;

XX DT 24-DEC-1997 (First entry)

XX DE Human SK29-MEL tyrosinase.

XX KW Tyrosine; tumour rejection antigen; TRAP; human leukocyte antigen;

XX HLA-B44; SK29-MEL; major histocompatibility complex; MHC;

XX cellular abnormality; melanoma; autoimmune disease; gene therapy;

XX diagnosis.

XX OS Homo sapiens.

XX PH Key

FT Peptide

PT Protein

FT Misc-difference

FT FT

CC This polypeptide comprises a human tyrosinase whose sequence was deduced  
 CC from a cDNA clone (see AAT75678) which was isolated from cell line  
 CC SK29-MEL.1 following a screen for clones that stimulated  
 CC cytolytic T cell lines CTL 210/9 and CTL IVSB. Human tyrosinase acts as a  
 CC tumour rejection antigen precursor and is processed to form a peptide  
 CC that is presented on the surface of a cell in combination with HLA-A2, thereby stimulating lysis by CTL  
 CC clones. Methods are claimed for identifying individuals having abnormal  
 CC cells that present complexes of the tumour rejection antigen and HLA-B44,  
 CC for treating such individuals (e.g. by administering vectors that code  
 CC for human tyrosinase and an HLA-B44 molecule), for isolating cytolytic T  
 CC cells specific for the complex of HLA-B44 and the peptide, and for  
 CC identifying abnormal cells. The methods can be used to treat tumours,  
 CC such as melanoma, autoimmune disorders, etc  
 XX

SQ Sequence 531 AA;

Query Match 100.0%; Score 83; DB 2; Length 531;

Best Local Similarity 100.0%; Pred. No. 9.3e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0;

Gaps 0;

Sequence 531 AA;

Query Match 100.0%; Score 83; DB 2; Length 531;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0;

Gaps 0;

Sequence 531 AA;

Query Match 100.0%; Score 83; DB 2; Length 531;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0;

Gaps 0;

RESULT 39

AAW38165 standard; protein; 560 AA.

ID AAW38165

XX AC AAW38165;

XX DT 13-MAR-1998 (first entry)

XX ID AAW38165

XX XX

XX DT 13-MAR-1998 (first entry)

XX XX

XX DE Human tyrosinase.

XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;

XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;

XX KW tyrosinase.

XX XX

XX OS Homo sapiens.

XX XX

XX DE Human tyrosinase.

XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;

XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;

XX KW tyrosinase.

XX XX

XX OS Homo sapiens.

XX XX

XX DE Human tyrosinase.

XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;

XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;

XX KW tyrosinase.

XX XX

XX OS Homo sapiens.

XX XX

XX DE Human tyrosinase.

XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;

XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;

XX KW tyrosinase.

XX XX

XX OS Homo sapiens.

XX XX

XX DE Human tyrosinase.

XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;

XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;

XX KW tyrosinase.

XX XX

XX OS Homo sapiens.

XX XX

XX DE Human tyrosinase.

XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;

XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;

XX KW tyrosinase.

XX XX

XX OS Homo sapiens.

XX XX

XX DE Human tyrosinase.

XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;

XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;

XX KW tyrosinase.

XX XX

XX OS Homo sapiens.

XX XX

XX DE Human tyrosinase.

XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;

XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;

XX KW tyrosinase.

XX XX

XX OS Homo sapiens.

XX XX

XX DE Human tyrosinase.

XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;

XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;

XX KW tyrosinase.

XX XX

XX OS Homo sapiens.

XX XX

XX DE Human tyrosinase.

XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;

XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;

XX KW tyrosinase.

XX XX

XX OS Homo sapiens.

XX XX

XX DE Human tyrosinase.

XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;

XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;

XX KW tyrosinase.

XX XX

XX OS Homo sapiens.

XX XX

XX DE Human tyrosinase.

XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;

XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;

XX KW tyrosinase.

XX XX

XX OS Homo sapiens.

XX XX

XX DE Human tyrosinase.

XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;

XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;

XX KW tyrosinase.

XX XX

XX OS Homo sapiens.

XX XX

XX DE Human tyrosinase.

XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;

XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;

XX KW tyrosinase.

XX XX

XX OS Homo sapiens.

XX XX

XX DE Human tyrosinase.

XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;

XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;

XX KW tyrosinase.

XX XX

XX OS Homo sapiens.

XX XX

XX DE Human tyrosinase.

XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;

XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;

XX KW tyrosinase.

XX XX

XX OS Homo sapiens.

XX XX

XX DE Human tyrosinase.

XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;

XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;

XX KW tyrosinase.

XX XX

XX OS Homo sapiens.

XX XX

XX DE Human tyrosinase.

XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;

XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;

XX KW tyrosinase.

XX XX

XX OS Homo sapiens.

XX XX

XX DE Human tyrosinase.

XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;

XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;

XX KW tyrosinase.

XX XX

XX OS Homo sapiens.

XX XX

XX DE Human tyrosinase.

XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;

XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;

XX KW tyrosinase.

XX XX

XX OS Homo sapiens.

XX XX

XX DE Human tyrosinase.

XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;

XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;

XX KW tyrosinase.

XX XX

XX OS Homo sapiens.

XX XX

XX DE Human tyrosinase.

XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;

XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;

XX KW tyrosinase.

XX XX

XX OS Homo sapiens.

XX XX

XX DE Human tyrosinase.

XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;

XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;

XX KW tyrosinase.

XX XX

XX OS Homo sapiens.

XX XX

XX DE Human tyrosinase.

XX KW Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;

XX KW melanocyte; biosynthesis; determination; Northern blot analysis; probe;

XX KW tyrosinase.

XX XX

XX OS Homo sapiens.

XX XX

CC can be determined by subjecting human melanocyte RNA to a Northern blot analysis, using the cDNA as a probe

CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania, Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is a savine protein of the invention

XX	Sequence 560 AA;
	Query Match 100.0%; Score 83; DB 2; Length 560;
	Best Local Similarity 100.0%; Pred. No. 9.9e-05;
	Matches 15; Conservative 0; N mismatches 0;
	Indels 0; Gaps 0;
QY	1 DYSYLQDSDPDSFQD 15
Db	446 DYSYLQDSDPDSFQD 460

## RESULT 40

AAU55008 ID AAU55008 standard; protein; 5546 AA.

XX

AC AAU85008;

XX

DT 08-MAY-2002 (first entry)

XX DE Human melanocyte differentiation antigens savine.

XX KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;

KW viral infection; human immunodeficiency virus; melanoma;

KW bacterial infection; Salmonella; Legionella; parasitic infection;

KW Trypanosoma; Toxoplasma; Giardia.

XX OS Homo sapiens.

OS Synthetic.

XX PN WO200190197-A1.

XX PD 29-NOV-2001.

XX PF 25-MAY-2001; 2001WO-AU0000622.

XX PR 26-MAY-2000; 2000AU-00007761.

XX (AUSU ) UNIV AUSTRALIAN NAT.

XX PI Thomson SA, Ramshaw IA;

XX DR 2002-147575/19.

XX N-PSDB; AERK36828.

XX New synthetic polypeptides having several different segments of at least PT one parent polypeptide linked together differently compared to the PT linkage in the parent polypeptide, for inducing immune response against a PT pathogen or cancer.

XX PS Example 3; Fig 27; 364pp; English.

XX The invention relates to a new synthetic polypeptide (I) comprising CC several different segments of at least one parent polypeptide linked CC together in a different relationship relative to their linkage in the CC parent polypeptide to impede, abrogate or otherwise alter at least one CC function associated with the parent polypeptide and for inducing an CC immune response against a pathogen or cancer. Also included are a CC synthetic polynucleotide encoding and a computer system for designing the CC synthetic polypeptides. The synthetic polypeptides and polynucleotides CC are referred to as a Savine. The synthetic polypeptide is useful for CC modulating immune responses preferably directed against a pathogen or a CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver, CC oesophagus, brain, testicle, uterus), as potentiating agents. CC Compositions comprising the polypeptide may be used in the treatment or CC prophylaxis against viral (such as infections caused by HIV (human CC immunodeficiency virus), hepatitis, Japanese encephalitis virus, Epstein-Barr virus and respiratory syncytial virus), bacterial CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus, CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic

CC	Sequence 5546 AA;
	Query Match 100.0%; Score 83; DB 5; Length 5546;
	Best Local Similarity 100.0%; Pred. No. 0.0013;
	Matches 15; Conservative 0; N mismatches 0;
	Indels 0; Gaps 0;
QY	1 DYSYLQDSDPDSFQD 15
Db	75 DYSYLQDSDPDSFQD 89

Search completed: June 3, 2004, 17:10:09

Job time : 57 secs



Result No.	Score	Query Match	Length	DB ID	Description	Score 83:	DB 9:	Length 15;
1	83	100.0	15	9	US-09-923-81-26	Sequence 26, Appl	0;	
2	83	100.0	15	9	US-09-766-89A-38	Sequence 38, Appl	0;	
3	83	100.0	15	12	US-10-218-095-33	Sequence 33, Appl	0;	
4	83	100.0	15	14	US-10-161-097-25	Sequence 25, Appl	0;	
5	83	100.0	15	14	US-10-170-932-67	Sequence 67, Appl	0;	
6	83	100.0	30	12	US-10-296-734-1030	Sequence 1030, Appl	0;	
7	83	100.0	43	16	US-10-447-161-142	Sequence 142, Appl	0;	
8	83	100.0	529	12	US-10-296-734-820	Sequence 820, Appl	0;	
9	83	100.0	529	12	US-10-253-886-487	Sequence 487, Appl	0;	
10	83	100.0	529	13	US-10-011-436-4	Sequence 4, Appl	0;	
11	83	100.0	529	15	US-10-026-066-4	Sequence 4, Appl	0;	
12	83	100.0	529	15	US-10-117-937-2	Sequence 2, Appl	0;	
13	83	100.0	529	15	US-10-245-871-487	Sequence 1210, Appl	0;	
14	83	100.0	5516	12	US-10-296-734-1210	Sequence 1032, Appl	0;	
15	77	92.8	30	12	US-10-296-734-1032	Sequence 92.8, Appl	0;	

%  
SUMMARIES

RESULT 1	US-09-923-831-26	SEQUENCE 26, Application US/09923831	PATENT NO. US20020115142A1
i GENERAL INFORMATION:			
i APPLICANT: Martelange, Valérie			
i DE SMET, Charles			
i APPLICANT: Boon-Falleur, Thierry			
i TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR			
i FILE REFERENCE: L04617054			
i CURRENT APPLICATION NUMBER: US-09-923, 831			
i CURRENT FILING DATE: 2001-08-07			
i PRIOR APPLICATION NUMBER: 09183, 705			
i PRIOR FILING DATE: 2001-10-30			
i NUMBER OF SEQ ID NOS: 43			
i SEQ ID NO: 26			
i LENGTH: 15			
i TYPE: PRT			
i ORGANISM: Homo sapiens			

RESULT 2  
US-09-766-89A-38

RESULT 2	US-09-766-89A-38	SEQUENCE 38, Application US/09766889A	PATENT NO. US2002016454A1
i GENERAL INFORMATION:			
i APPLICANT: Luitjen, Rosalie			
i APPLICANT: Boon-Falleur, Thierry			
i APPLICANT: van der Bruggen, Pierre			

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

APPLICANT: Stroobant, Vincent  
 APPLICANT: Demotte, Nathalie  
 APPLICANT: Schultz, Erwin  
 TITLE OF INVENTION: IMAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44  
 FILE REFERENCE: L0461-/T104  
 CURRENT APPLICATION NUMBER: US/09/766,889A  
 CURRENT FILING DATE: 2001-01-19  
 PRIOR APPLICATION NUMBER: US 60/177,242  
 PRIOR FILING DATE: 2000-01-20  
 PRIOR APPLICATION NUMBER: US 60/243,212  
 PRIOR FILING DATE: 2000-10-25  
 NUMBER OF SEQ ID NOS: 59  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 38  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-766-889A-38

Query Match		Score 83; DB 9; Length 15;	
Best Local Similarity	Matches 15;	Pred. No. 3.8e-06;	Indels 0;
Mismatches 0;	Conservative 0;	Gaps 0;	
Qy 1 DYSYLOQDSDPDSFQD 15			
Db 1 DYSYLOQDSDPDSFQD 15			

RESULT 3  
 US-10-218-095-33  
 Sequence 33, Application US/10218095  
 Publication No. US20040033541A1  
 GENERAL INFORMATION:  
 APPLICANT: Zhang, Yi  
 APPLICANT: Stroobant, Vincent  
 APPLICANT: Russo, Vincenzo  
 APPLICANT: Boon-Falleur, Thierry  
 APPLICANT: van der Bruggen, Pierre  
 TITLE OF INVENTION: MAGE-A4 ANTIGENIC PEPTIDES AND USES THEREOF  
 FILE REFERENCE: L00461/70137  
 CURRENT APPLICATION NUMBER: US/10/218,095  
 CURRENT FILING DATE: 2002-08-13  
 NUMBER OF SEQ ID NOS: 63  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 33  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-218-095-33

Query Match		Score 83; DB 12; Length 15;	
Best Local Similarity	Matches 15;	Pred. No. 3.8e-06;	Indels 0;
Mismatches 0;	Conservative 0;	Gaps 0;	
Qy 1 DYSYLOQDSDPDSFQD 15			
Db 1 DYSYLOQDSDPDSFQD 15			

RESULT 4  
 US-10-161-097-25  
 Sequence 25, Application US/10161097  
 Publication No. US20030096404A1  
 GENERAL INFORMATION:  
 APPLICANT: ROSENWEIG, Michael  
 APPLICANT: PYKETT, Mark J.  
 APPLICANT: SCADDEN, David T.  
 APPLICANT: POZNANSKY, Mark C.  
 TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION  
 TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL  
 TITLE OF INVENTION: DEVICES  
 FILE REFERENCE: C1005/7012/KA/ERG  
 CURRENT APPLICATION NUMBER: US/10/161,097

CURRENT FILING DATE: 2002-05-31  
 PRIOR APPLICATION NUMBER: US/09/574,749  
 PRIOR FILING DATE: 2002-05-31  
 PRIOR APPLICATION NUMBER: US 60/107,972  
 PRIOR FILING DATE: 1998-11-12  
 PRIOR APPLICATION NUMBER: PCT/US99/26795  
 PRIOR FILING DATE: 1999-11-12  
 PRIOR APPLICATION NUMBER: US 09/524,749  
 PRIOR FILING DATE: 2000-05-18  
 NUMBER OF SEQ ID NOS: 58  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 25  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Homo Sapiens source  
 US-10-161-097-25

Query Match		Score 83; DB 14; Length 15;	
Best Local Similarity	Matches 15;	Pred. No. 3.8e-06;	Indels 0;
Mismatches 0;	Conservative 0;	Gaps 0;	
Qy 1 DYSYLOQDSDPDSFQD 15			
Db 1 DYSYLOQDSDPDSFQD 15			

RESULT 5  
 US-10-170-832-67  
 Sequence 67, Application US/10170832  
 Publication No. US20030170792A1  
 GENERAL INFORMATION:  
 APPLICANT: Chaux, Pascal  
 APPLICANT: Vantomme, Valrie  
 APPLICANT: Stroobant, Vincent  
 APPLICANT: Boon-Falleur, Thierry  
 APPLICANT: van der Bruggen, Pierre  
 APPLICANT: Thielmanns, Kris  
 APPLICANT: Cortahls, Jurgen  
 TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
 FILE REFERENCE: L0461/7052  
 CURRENT APPLICATION NUMBER: US/10/170,832  
 CURRENT FILING DATE: 2002-06-12  
 PRIOR APPLICATION NUMBER: US/09/166,448  
 PRIOR FILING DATE: 1998-10-05  
 NUMBER OF SEQ ID NOS: 81  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 67  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-170-832-67

Query Match		Score 83; DB 14; Length 15;	
Best Local Similarity	Matches 15;	Pred. No. 3.8e-06;	Indels 0;
Mismatches 0;	Conservative 0;	Gaps 0;	
Qy 1 DYSYLOQDSDPDSFQD 15			
Db 1 DYSYLOQDSDPDSFQD 15			

RESULT 6  
 US-10-236-734-1030  
 Sequence 1030, Application US/10236734  
 Publication No. US20040054137A1  
 GENERAL INFORMATION:  
 APPLICANT: Thompson, Scott A  
 APPLICANT: Ramsaw, Ian A  
 TITLE OF INVENTION: Synthetic molecules and uses therefor  
 FILE REFERENCE: Savine  
 CURRENT APPLICATION NUMBER: US/10/296,734

CURRENT FILING DATE: 2003-08-04  
; PRIORITY APPLICATION NUMBER: AU PQ7761/00  
; PRIOR FILING DATE: 2000-05-26  
; NUMBER OF SEQ ID NOS: 1507  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 1330  
; LENGTH: 30  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: tyros segment 3.0  
US-10-296-734-1030

Query Match  
Best Local Similarity 100.0%; Score 83; DB 12; Length 30;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DYSYIQLQDSDPDSFQD 15  
Db 15 DYSYIQLQDSDPDSFQD 29

RESULT 7  
US-10-447-161-142  
; Sequence 142 Application US/10447161  
; Publication No. US200401023314A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Rong-fu  
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis  
; FILE REFERENCE: HO-P02494US1  
; CURRENT APPLICATION NUMBER: US/10/447,161  
; CURRENT FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: 60/383,530  
; PRIOR FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 148  
; SEQ ID NO: 142  
; LENGTH: 43  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
US-10-447-161-142

Query Match  
Best Local Similarity 100.0%; Score 83; DB 16; Length 43;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DYSYIQLQDSDPDSFQD 15  
Db 16 DYSYIQLQDSDPDSFQD 30

RESULT 8  
US-10-296-734-820  
; Sequence 820 Application US/10296734  
; Publication No. US20040054137A1  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Scott A  
; APPLICANT: Ramsdaw, Ian A  
; TITLE OF INVENTION: Synthetic molecules and uses therefor  
; FILE REFERENCE: Savine  
; CURRENT APPLICATION NUMBER: US/10/296,734  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: AU PQ7761/00  
; NUMBER OF SEQ ID NOS: 1507  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 820  
; LENGTH: 529  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:

; OTHER INFORMATION: Tyros consensus polypeptide  
US-10-296-734-820  
Query Match 100.0%; Score 83; DB 12; Length 529;  
Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DYSYIQLQDSDPDSFQD 15  
Db 448 DYSYIQLQDSDPDSFQD 462

RESULT 9  
US-10-253-286-487  
; Sequence 487 Application US/10253286  
; Publication No. US2004005881A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: REH-2015  
; CURRENT APPLICATION NUMBER: US/10/253,286  
; CURRENT FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 09/396,813  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 905  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 487  
; LENGTH: 529  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-253-286-487

Query Match 100.0%; Score 83; DB 12; Length 529;  
Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DYSYIQLQDSDPDSFQD 15  
Db 448 DYSYIQLQDSDPDSFQD 462

RESULT 10  
US-10-011-436-4  
; Sequence 4 Application US/1001436  
; Publication No. US20020128200A1  
; GENERAL INFORMATION:  
; APPLICANT: Bon-Falleur, Thierry; Brichard, Vincent; Van Pel,  
; ALINE; Lethe, Bernard  
; DEPLAEN, Etienne; Coulie, Pierre; Renauld, Jean Christophe; Wolfel,  
; TITLE OF INVENTION: METHOD FOR IDENTIFYING INDIVIDUALS SUFFERING FROM  
; CELLULAR ABNORMALITY SOME OF WHOSE ABNORMAL CELLS PRESENT C  
; LEUKOCYTE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; STREET: Fulbright & Jaworski L.L.P.  
; CITY: 801 Pennsylvania Avenue N.W.  
; STATE: Washington District of Columbia  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.25inch, 1.44MB storage  
; OPERATING SYSTEM: IBM PS/2  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; FILING DATE: 11-Dec-2001

CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/511,011  
 FILING DATE: 5-AUGUST-1995  
 APPLICATION NUMBER: 08/054,714  
 FILING DATE: 28-APRIL-1993  
 APPLICATION NUMBER: 07/994,928  
 FILING DATE: 22-DECEMBER-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mary Anne Schoffield  
 REGISTRATION NUMBER: 36,669  
 REFERENCE/DOCKET NUMBER: LUD 5299.9 DIV CON  
 TELEPHONE: (202) 662-0200  
 TELEFAX: (202) 662-4643  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 529  
 TYPE: amino acids  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
 US-10-011-436-4

Query Match 100.0%; Score 83; DB 13; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 0.00017;  
 Matches 15; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 DYSYLOQSDPDSFQD 15  
 Db 448 DYSYLOQSDPDSFQD 462

RESULT 11  
 US-10-026-066-4  
 Sequence 4, Application US/10026066  
 Publication No. US20030215425A1  
 GENERAL INFORMATION:  
 APPLICANT: Simard, John J. L.  
 APPLICANT: Diamond, David C.  
 APPLICANT: Djiamond, David C.  
 TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN  
 PRESENTING CELLS  
 FILE REFERENCE: CTIIMM.21CPLIC

CURRENT APPLICATION NUMBER: US/10/026,066  
 CURRENT FILING DATE: 2001-12-07  
 PRIOR APPLICATION NUMBER: 09/556,074  
 PRIOR FILING DATE: 2000-04-28  
 PRIOR APPLICATION NUMBER: 09/550,465  
 PRIOR FILING DATE: 2000-04-28  
 PRIOR APPLICATION NUMBER: 09/556,1,572  
 PRIOR FILING DATE: 2000-04-28  
 PRIOR APPLICATION NUMBER: 09/556,1,571  
 PRIOR FILING DATE: 2000-04-28  
 PRIOR APPLICATION NUMBER: PCT/US01/13906  
 PRIOR FILING DATE: 2001-04-27  
 NUMBER OF SEQ ID NOS: 89  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 4  
 LENGTH: 529  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-026-066-4

Query Match 100.0%; Score 83; DB 15; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 0.00017;  
 Matches 15; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 DYSYLOQSDPDSFQD 15  
 Db 448 DYSYLOQSDPDSFQD 462

RESULT 12  
 US-10-117-937-2  
 Sequence 2, Application US/10117937  
 Publication No. US2003022039A1  
 GENERAL INFORMATION:  
 APPLICANT: CTL IMMUNO THERAPIES CORP.  
 APPLICANT: SIMARD, JOHN, J.L.  
 APPLICANT: DIAMOND, DAVID, C.  
 APPLICANT: LIU, Liping  
 APPLICANT: XIE, Zhiqiong  
 TITLE OF INVENTION: EPITOPE SEQUENCES  
 FILE REFERENCE: CTIIMM.027A  
 CURRENT APPLICATION NUMBER: US/10/117,937  
 CURRENT FILING DATE: 2002-04-04  
 PRIOR APPLICATION NUMBER: US 60/282,211  
 PRIOR FILING DATE: 2001-04-06  
 PRIOR APPLICATION NUMBER: US 60/337,017  
 PRIOR FILING DATE: 2001-11-07  
 PRIOR APPLICATION NUMBER: US 60/363,210  
 PRIOR FILING DATE: 2002-03-07  
 NUMBER OF SEQ ID NOS: 602  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 2  
 LENGTH: 529  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-117-937-2

Query Match 100.0%; Score 83; DB 15; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 0.00017;  
 Matches 15; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 DYSYLOQSDPDSFQD 15  
 Db 448 DYSYLOQSDPDSFQD 462

RESULT 13  
 US-10-245-871-487  
 Sequence 487, Application US/10245871  
 Publication No. US20030235594A1  
 GENERAL INFORMATION:  
 APPLICANT: HUMPHREYS, ROBERT  
 APPLICANT: XU, MINZHEN  
 TITLE OF INVENTION: Ti-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
 FILE REFERENCE: REH-2013  
 CURRENT APPLICATION NUMBER: US/10/245,871  
 CURRENT FILING DATE: 2003-01-09  
 PRIOR APPLICATION NUMBER: 10/197,000  
 PRIOR FILING DATE: 2002-07-17  
 PRIOR APPLICATION NUMBER: 09/396,813  
 PRIOR FILING DATE: 1999-09-14  
 NUMBER OF SEQ ID NOS: 905  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 487  
 LENGTH: 529  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-245-871-487

Query Match 100.0%; Score 83; DB 15; Length 529;  
 Best Local Similarity 100.0%; Pred. No. 0.00017;  
 Matches 15; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 DYSYLOQSDPDSFQD 15  
 Db 448 DYSYLOQSDPDSFQD 462

RESULT 14  
 US-10-296-734-1210  
 Sequence 1210, Application US/10296734  
 Publication No. US20040054137A1  
 GENERAL INFORMATION:

RESULT 15

; APPLICANT: Thompson, Scott A  
 ; APPLICANT: Ramshaw, Ian A  
 ; TITLE OF INVENTION: Synthetic molecules and uses therefor  
 ; FILE REFERENCE: Savine  
 ; CURRENT APPLICATION NUMBER: US/10/296,734  
 ; CURRENT FILING DATE: 2003-08-04  
 ; PRIOR APPLICATION NUMBER: AU PQ7761/00  
 ; PRIOR FILING DATE: 2000-05-26  
 ; NUMBER OF SEQ ID NOS: 1507  
 ; SEQ ID NO 1240  
 ; SOFTWARE: PatentIn version 3.2  
 ; LENGTH: 5546  
 ; TYPE: PRT  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: Differentiation svaine  
 US-10-296-734-1210

	Query Match	Score	DB	Length
Matches	Best Local Similarity	100.0%	12	5546;
Qy	15	0	0	0;
Db	DYSYLOPQDSDPSFQD 15 75 DYSYLOPQDSDPSFQD 89	0	0	0;

RESULT 15  
 US-10-296-734-1032  
 ; Sequence 1032, Application US/10296734  
 ; Publication No. US2004010054-37A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Thompson, Scott A  
 ; APPLICANT: Ramshaw, Ian A  
 ; TITLE OF INVENTION: Synthetic molecules and uses therefor  
 ; FILE REFERENCE: Savine  
 ; CURRENT APPLICATION NUMBER: US/10/296,734  
 ; CURRENT FILING DATE: 2003-08-04  
 ; PRIOR APPLICATION NUMBER: AU PQ7761/00  
 ; PRIOR FILING DATE: 2000-05-26  
 ; NUMBER OF SEQ ID NOS: 1507  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 1032  
 ; LENGTH: 30  
 ; TYPE: PRT  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: tyros segment 31

US-10-296-734-1032

	Query Match	Score	DB	Length
Matches	Best Local Similarity	92.8%	12	30;
Qy	2 YSYLOPQDSDPSFQD 15	0	0	0;
Db	1 YSYLOPQDSDPSFQD 14	0	0	0;

Search completed: June 3, 2004, 15:24:23  
 Job time : 40 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	15	2 US-09-036-582-23	Sequence 23, Appl
2	83	100.0	15	3 US-09-183-106-26	Sequence 26, Appl
3	83	100.0	15	4 US-09-166-448-67	Sequence 67, Appl
4	83	100.0	15	5 US-09-567-995-26	Sequence 26, Appl
5	83	100.0	15	6 US-09-165-863-23	Sequence 23, Appl
6	83	100.0	15	7 US-09-697-884-67	Sequence 67, Appl
7	83	100.0	15	8 US-09-289-350-29	Sequence 23, Appl
8	83	100.0	15	9 US-09-1574-749B-5	Sequence 25, Appl
9	83	100.0	15	10 US-09-318-141-23	Sequence 23, Appl
10	83	100.0	15	11 US-09-169-717E-39	Sequence 29, Appl
11	83	100.0	15	12 US-07-891-942G-10	Sequence 10, Appl
12	83	100.0	15	13 US-07-891-942G-8	Sequence 8, Appl
13	83	100.0	15	14 US-08-370-909-19	Sequence 19, Appl
14	83	100.0	15	15 US-08-504-048-8	Sequence 8, Appl
15	83	100.0	15	16 US-09-341-9822-1	Sequence 1, Appl
16	83	100.0	15	17 US-09-169-717E-39	Sequence 39, Appl
17	83	100.0	15	18 US-10-011-436-4	Sequence 4, Appl
18	83	100.0	15	19 US-08-540-922D-12	Sequence 12, Appl
19	83	100.0	15	20 US-07-891-942G-5	Sequence 5, Appl
20	70	84.3	13	21 US-08-902-516-42	Sequence 42, Appl
21	70	84.3	13	22 US-09-847-185-42	Sequence 42, Appl
22	70	84.3	13	23 US-01-729-113	Sequence 113, Appl
23	62	74.7	19	24 US-08-504-048-4	Sequence 4, Appl
24	59	71.1	12	25 US-09-341-982-3	Sequence 3, Appl
25	55	66.3	11	26 US-09-341-982-5	Sequence 5, Appl
26	48	57.8	696	27 US-09-907-794A-91	Sequence 91, Appl
27	48	57.8	696	28 US-09-905-125A-91	Sequence 91, Appl

Query Match 100.0%; Score 83; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYIQLQDSDPDSFQD 15  
 Db 1 DYSYIQLQDSDPDSFQD 15

RESULT 3 

Sequence 67, Application US/0916448  
 Patent No. 6291430  
 GENERAL INFORMATION:  
 APPLICANT: Chaux, Pascal  
 APPLICANT: Vantomme, Valrie  
 APPLICANT: Stroobant, Vincent  
 APPLICANT: Boon-Falleur, Thierry  
 APPLICANT: van der Bruggen, Pierre  
 APPLICANT: Thielemans, Kris  
 APPLICANT: Cortahs, Jurgen  
 TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
 FILE REFERENCE: L0461/7052  
 CURRENT APPLICATION NUMBER: US/09/166,448  
 CURRENT FILING DATE: 1998-10-05  
 NUMBER OF SEQ ID NOS: 81  
 SOFTWARE: FastSEQ for Windows version 3.0  
 SEQ ID NO 67  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-166-448-67

Query Match 100.0%; Score 83; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYIQLQDSDPDSFQD 15  
 Db 1 DYSYIQLQDSDPDSFQD 15

RESULT 4 

US-09-567-995-26 

Sequence 26, Application US/095567995  
 GENERAL INFORMATION:  
 APPLICANT: Martelange, Valarie  
 APPLICANT: De Smet, Charles  
 APPLICANT: Boon-Falleur, Thierry  
 TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
 FILE REFERENCE: L0461/7054  
 CURRENT APPLICATION NUMBER: US/09/567,995  
 CURRENT FILING DATE: 2000-05-10  
 PRIOR APPLICATION NUMBER: 09/183,706  
 PRIOR FILING DATE: 1998-10-30  
 NUMBER OF SEQ ID NOS: 43  
 SEQ ID NO 26  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-567-995-26

Query Match 100.0%; Score 83; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYIQLQDSDPDSFQD 15  
 Db 1 DYSYIQLQDSDPDSFQD 15

RESULT 5 

US-09-289-350-23  
 Sequence 23, Application US/09289350

US-09-165-863-23 

Sequence 23, Application US/09165863  
 Patent No. 6467063  
 GENERAL INFORMATION:  
 APPLICANT: Lutten, Rosalie  
 APPLICANT: Duffour, Marie-Therese  
 APPLICANT: Demotte, Nathalie  
 APPLICANT: van der Bruggen, Pierre  
 APPLICANT: Cornelis, Guy  
 APPLICANT: Stroobant, Vincent  
 APPLICANT: Lurquin, Christophe  
 APPLICANT: Boon-Falleur, Thierry  
 APPLICANT: Chaux, Pascal  
 TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL  
 FILE REFERENCE: 11727  
 CURRENT APPLICATION NUMBER: US/09/165,863  
 CURRENT FILING DATE: 1999-10-02  
 NUMBER OF SEQ ID NOS: 45  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 23  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Human Tyrosinase peptide  
 US-09-165-863-23

Query Match 100.0%; Score 83; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYIQLQDSDPDSFQD 15  
 Db 1 DYSYIQLQDSDPDSFQD 15

RESULT 6 

US-09-697-884-67 

Sequence 67, Application US/09697884  
 Patent No. 646217  
 GENERAL INFORMATION:  
 APPLICANT: Vantomme, Valarie  
 APPLICANT: Stroobant, Vincent  
 APPLICANT: Boon-Falleur, Thierry  
 APPLICANT: van der Bruggen, Pierre  
 APPLICANT: Thielemans, Kris  
 APPLICANT: Cortahs, Jurgen  
 TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
 FILE REFERENCE: L0461/7052  
 CURRENT APPLICATION NUMBER: US/09/697,884  
 CURRENT FILING DATE: 2000-10-27  
 PRIOR APPLICATION NUMBER: 09/156,448  
 PRIOR FILING DATE: 1998-10-05  
 NUMBER OF SEQ ID NOS: 81  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO 67  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-697-884-67

OK

Query Match 100.0%; Score 83; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
 Matches 15; Conservative 0; Mismatches 0; Gaps 0;  
 SEQ ID NO: 25  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Homo Sapiens source

Db 1 DSYLQDSDPDSFQD 15

---

RESULT 8  
 US-09-574-749B-25  
 Sequence 25, Application US/09574749B  
 GENERAL INFORMATION:  
 Patent No. 6518299  
 APPLICANT: ROSENZWEIG, Michael  
 APPLICANT: PYKETT, Mark J.  
 APPLICANT: SCADDEN, David T.  
 APPLICANT: POZNANSKY, Mark C.  
 TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION  
 TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL  
 CURRENT APPLICATION NUMBER: US/09/574,749B  
 FILE REFERENCE: C1005/7012/KA/ERG  
 CURRENT FILING DATE: 2002-05-31  
 PRIOR APPLICATION NUMBER: US 60/107,972  
 PRIOR FILING DATE: 1998-11-12  
 PRIOR APPLICATION NUMBER: PCT/US99/26795  
 PRIOR FILING DATE: 1999-11-12  
 PRIOR APPLICATION NUMBER: US 09/524,749  
 PRIOR FILING DATE: 2000-05-18  
 NUMBER OF SEQ ID NOS: 58  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 25  
 LENGTH: 15  
 TYPE: PRT  
 FEATURE:  
 OTHER INFORMATION: Homo Sapiens source

Query Match 100.0%; Score 83; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
 Matches 15; Conservative 0; Mismatches 0; Gaps 0;  
 SEQ ID NO: 25  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Artificial Sequence

Db 1 DSYLQDSDPDSFQD 15

---

RESULT 9  
 US-09-318-141-23  
 Sequence 23, Application US/09318141  
 Patent No. 660506  
 GENERAL INFORMATION:  
 APPLICANT: van der Bruggen, Pierre  
 APPLICANT: Cornelis, Guy R.  
 TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS  
 FILE REFERENCE: 11154  
 CURRENT FILING DATE: 1999-05-14  
 EARLIER APPLICATION NUMBER: US 09/036,582  
 EARLIER FILING DATE: 1998-03-06  
 NUMBER OF SEQ ID NOS: 39  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 23  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Human Tyrosinase peptide

Db 1 DSYLQDSDPDSFQD 15

---

RESULT 10  
 US-09-169-717E-29  
 Sequence 29, Application US/09169717E  
 Patent No. 6667037  
 GENERAL INFORMATION:  
 APPLICANT: Ooms, Annie  
 APPLICANT: DeGiovanni, Gerard  
 APPLICANT: Morel, Sandra  
 APPLICANT: Van den Eynde, Benoit  
 APPLICANT: Boon-Falleur, Thierry  
 TITLE OF INVENTION: Isolater Peptides Which Bind To HLA-B35 Molecules,  
 TITLE OF INVENTION: Larger Peptides Which Contain These, Nucleic Acid  
 TITLE OF INVENTION: Molecules Encoding Peptides, And Uses Thereof  
 CURRENT APPLICATION NUMBER: US/09/169,717E  
 FILE REFERENCE: LUD5561  
 CURRENT FILING DATE: 1998-10-09  
 NUMBER OF SEQ ID NOS: 39  
 SEQ ID NO: 29  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 US-09-169-717E-29

Query Match 100.0%; Score 83; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
 Matches 15; Conservative 0; Mismatches 0; Gaps 0;

Db 1 DSYLQDSDPDSFQD 15

---

RESULT 11  
 US-07-891-942G-10  
 Sequence 10, Application US/07891942G  
 Patent No. 5679511  
 GENERAL INFORMATION:  
 APPLICANT: Kwon, Byoung Se

Query Match 100.0%; Score 83; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
 Matches 15; Conservative 0; Mismatches 0; Gaps 0;

Db 1 DSYLQDSDPDSFQD 15

TITLE OF INVENTION: cDNA CLONES FOR HUMAN TYROSINASE AND FOR  
 TITLE OF INVENTION: A REGULATORY PROTEIN IN THE MELANIN PROTEIN PATHWAY  
 NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Christopher A. Michaels, Barnard, Brown &  
 STREET: 306 East State Street; Suite 220  
 CITY: Ithaca  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 14850

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/891,942G  
 FILING DATE: 01-JUN-1992

CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 06/915,753  
 FILING DATE: 06-OCT-1986

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/362,847

ATTORNEY/AGENT INFORMATION:  
 NAME: Michaels, Christopher A  
 REGISTRATION NUMBER: 34,390  
 REFERENCE/DOCKET NUMBER: IND1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 607-273-1711  
 TELEFAX: 607-273-2609

SEQUENCE CHARACTERISTICS:  
 LENGTH: 508 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

RESULT 12  
 US-07-891-942G-8  
 Sequence 8 Application US/07891942G  
 Patent No. 5679511  
 GENERAL INFORMATION:  
 APPLICANT: Kwon, Byoung Se  
 TITLE OF INVENTION: cDNA CLONES FOR HUMAN TYROSINASE AND FOR  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Christopher A. Michaels, Barnard, Brown &  
 STREET: 306 East State Street; Suite 220  
 CITY: Ithaca  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 14850

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/891,942G  
 FILING DATE: 01-JUN-1992  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 06/915,753  
 FILING DATE: 06-OCT-1986

ATTORNEY/AGENT INFORMATION:  
 NAME: Michaels, Christopher A  
 REGISTRATION NUMBER: 34,390  
 REFERENCE/DOCKET NUMBER: IND1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 607-273-1711  
 TELEFAX: 607-273-2609

SEQUENCE CHARACTERISTICS:  
 LENGTH: 529 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

RESULT 13  
 US-08-370-909-19  
 Sequence 19 Application US/08370909  
 Patent No. 5143648  
 GENERAL INFORMATION:  
 APPLICANT: ROBBINS, PAUL F.; ROSENBERG,  
 ATTORNEY/AGENT INFORMATION:  
 NAME: ROBBINS, PAUL F.; ROSENBERG,  
 ATTORNEY/AGENT INFORMATION:  
 NAME: STEVEN A.  
 TITLE OF INVENTION: P15 AND TYROSINASE  
 TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC  
 TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC  
 NUMBER OF SEQUENCES: 23  
 CURRENT APPLICATION DATA:  
 ADDRESSER: MORGAN & FINNEGAN, L.L.P.  
 STREET: 345 PARK AVENUE  
 CITY: NEW YORK  
 STATE: NEW YORK  
 COUNTRY: USA  
 ZIP: 10154  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/370,909  
 FILING DATE: 10-JAN-1995  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: CAROL M. GRUPPI  
 REGISTRATION NUMBER: 37,341  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 758-4800  
 TELFAX: (212) 751-6849  
 TELEX: 421792  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 529  
 TYPE: AMINO ACID  
 STRANDEDNESS: UNKNOWN

RESULT 14  
 TOPOLOGY: UNKNOWN  
 MOLECULE TYPE: PROTEIN  
 US-08-370-909-19

Query Match Score: 83; DB: 2; Length: 529;  
 Best Local Similarity: 100.0%; Pred. No.: 1e-05;  
 Matches: 15; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 DYSYLOQSDPDSFQD 15  
 Db 448 DYSYLOQSDPDSFQD 462

RESULT 14  
 US-08-504-048-8

Sequence 8, Application US/08504048  
 Patent No. 5843674

GENERAL INFORMATION:  
 APPLICANT: TAKIMOTO, Hiroyuki  
 NUMBER OF SEQUENCES: 9

APPLICANT: SUZUKI, Satoshi  
 NUMBER OF SEQUENCES: 9

APPLICANT: SHIBATA, Koushi  
 NUMBER OF SEQUENCES: 9

APPLICANT: MASUI, Shigeki  
 NUMBER OF SEQUENCES: 9

TITLE OF INVENTION: ANTI-HUMAN TYROSINASE  
 TITLE OF INVENTION: MONOClonal ANTIBODY

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Knobbe, Martens, Olson & Bear  
 STREET: 620 Newport Center Drive 16th Floor  
 CITY: Newport Beach  
 STATE: CA  
 COUNTRY: U.S.A.  
 ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/504,048  
 FILING DATE:  
 CLASSIFICATION: 436  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Altman, Daniel E  
 REGISTRATION NUMBER: 34,115  
 REGISTRATION INFORMATION:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 714-760-0404  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 529 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: internal  
 ORIGINAL SOURCE:  
 US-08-504-048-8

RESULT 15  
 US-09-341-982-1

Sequence 1, Application US/09341982  
 Patent No. 658671

GENERAL INFORMATION:  
 APPLICANT: SITNGLUFF, Craig L.  
 APPLICANT: HUNN, Donald F.  
 APPLICANT: ENGELHARD, Victor H.  
 APPLICANT: KITTLESEN, David  
 TITLE OF INVENTION: CYTOTOXIC LYMPHOCYTES, AND USES THEREFOR  
 FILE REFERENCE: SITNGLUFF-3B  
 CURRENT APPLICATION NUMBER: US/09/341,982  
 CURRENT FILING DATE: 1999-09-20  
 EARLIER APPLICATION NUMBER: PCT/US98/01592  
 EARLIER FILING DATE: 1998-01-29  
 EARLIER APPLICATION NUMBER: 60/037,781  
 EARLIER FILING DATE: 1997-01-31  
 NUMBER OF SEQ ID NOS: 104  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 1  
 LENGTH: 529  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-341-982-1

Query Match Score: 83; DB: 4; Length: 529;  
 Best Local Similarity: 100.0%; Pred. No.: 1e-05;  
 Matches: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 DYSYLOQSDPDSFQD 15  
 Db 448 DYSYLOQSDPDSFQD 462

RESULT 16  
 US-09-169-717E-39

Sequence 39, Application US/09169717E  
 Patent No. 6667037

GENERAL INFORMATION:  
 APPLICANT: Ooms, Annie  
 APPLICANT: Degiovanni, Gerard  
 APPLICANT: Morel, Sandra  
 APPLICANT: Van den Bynde, Benoit  
 APPLICANT: Boon-Faillieu, Thierry

TITLE OF INVENTION: Isolator Peptides Which Bind To HLA-B35 Molecules,  
 Larger Peptides Which Contain These, Nucleic Acid  
 TITLE OF INVENTION: Molecules Encoding Peptides, And Uses Thereof  
 FILE REFERENCE: LUDD561  
 CURRENT APPLICATION NUMBER: US/09/169,717E  
 NUMBER OF SEQ ID NOS: 39  
 SEQ ID NO: 39

Query Match Score: 83; DB: 4; Length: 529;  
 Best Local Similarity: 100.0%; Pred. No.: 1e-05;  
 Matches: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 DYSYLOQSDPDSFQD 15  
 Db 448 DYSYLOQSDPDSFQD 462

RESULT 17  
 US-10-011-436-4

Sequence 4, Application US/10011436  
 Patent No. 6669946

Query Match Score: 83; DB: 2; Length: 529;  
 Best Local Similarity: 100.0%; Pred. No.: 1e-05;  
 Matches: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 DYSYLOQSDPDSFQD 15  
 Db 448 DYSYLOQSDPDSFQD 462

GENERAL INFORMATION:

APPLICANT: Boon-Falleur, Thierry; Brichard, Vincent; Van Pel, Aline;

ADDRESSEE: Coulie, Pierre; Renaud, Jean Christophe; Wolfe, Lethe, Bernard

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEES: Fulbright & Jaworski L.L.P.

STREET: 801 Pennsylvania Avenue N.W.

CITY: Washington

STATE: District of Columbia

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Disquette, 3.25inch, 1.44MB storage

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/011,436

FILING DATE: 11-DEC-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/511,011

FILING DATE: 5-AUGUST-1995

APPLICATION NUMBER: 08/054,714

FILING DATE: 28-APRIL-1993

APPLICATION NUMBER: 07/1994,928

FILING DATE: 22-DECEMBER-1992

ATTORNEY/AGENT INFORMATION:

NAME: Mary Anne Schofield

REGISTRATION NUMBER: 36,669

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 662-0200

TELEFAX: (202) 662-4643

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 529

TYPE: amino acids

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-011-436-4

Query Match Score 83; DB 4; Length 529;

Best Local Similarity 100.0%; Pred. No. 1e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSYLQDSDPSFQD 15

Db 448 DSYLQDSDPSFQD 462

RESULT 18

US-08-540-922D-12

Patent No. 6284476

GENERAL INFORMATION:

APPLICANT: Boon-Falleur, Thierry; Brichard, Vincent; Van Pel, Aline; De Plaein, Etienne; Coulie, Pierre;

APPLICANT: Renaud, Jean-Christophe; Wolfe, Thomas; and

APPLICANT: Lethe, Bernard.

TITLE OF INVENTION: METHOD OF IDENTIFYING INDIVIDUALS SUFFERING FROM A CELLULAR ABNORMALITY, SOME OF WHOM ARE ABNORMAL CELLS PRESENT COMPLEXES OF HUMAN LEUKOCYTE ANTIGEN TYROSINASE DERIVED PEPTIDES, AND METHODS FOR TREATING SAID INDIVIDUALS

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEES: Felife & Lynch

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/540,922D

FILING DATE: October 11, 1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/054,714

FILING DATE: 28 April 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/1994,928

FILING DATE: 22 December 1992

ATTORNEY/AGENT INFORMATION:

NAME: Mary Anne Schofield

REGISTRATION NUMBER: 36,669

REFERENCE/DOCKET NUMBER: IUD 5299.5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 638-3684

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 537

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-540-922D-12

RESULT 19

US-07-891-942G-5

Sequence 5, Application US/07891942G

Patent No. 5579511

GENERAL INFORMATION:

APPLICANT: Kwon, Byoung Se

TITLE OF INVENTION: cDNA CLONES FOR HUMAN TYROSINASE AND FOR TITLE OF INVENTION: A REGULATORY PROTEIN IN THE MELANIN PROTEIN PATHWAY

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEES: Christopher A. Michaels, Barnard, Brown & Michaels

STREET: 306 East State Street, Suite 220

CITY: Ithaca

STATE: NY

COUNTRY: USA

ZIP: 14850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.3.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/891,942G

FILING DATE: 01-JUN-1992

CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 06/915,753  
 FILING DATE: 06-OCT-1986  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 07/362,847  
 FILING DATE: 07-JUN-1989  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Michael S, Christopher A  
 REGISTRATION NUMBER: 34,390  
 REFERENCE/DOCKET NUMBER: IND1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 607-273-1711  
 TELEFAX: 607-273-2609  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 560 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-07-891-942G-5

Query Match 100.0%; Score 83; DB 1; Length 560;  
 Best Local Similarity 100.0%; Pred. No. 1e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 DYSYIQLQDSDPSFQD 15  
 Db 446 DYSYIQLQDSDPSFQD 460

## RESULT 20

US-08-902-516-42  
 Sequence 42, Application US/08902516  
 Patent No. 589132  
 GENERAL INFORMATION:  
 APPLICANT: Soo Hoo, William  
 TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
 COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
 SYSTEM  
 TITLE OF INVENTION:  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CAMPBELL & FLORES, LLP  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTY: United States  
 ZIP: 92121  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/902,516  
 FILING DATE: 29-JUL-1997  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Kathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-IM 2442  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)535-9001  
 TELEFAX: (619)535-8949  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-902-516-42

Query Match 84.3%; Score 70; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;



GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: June 3, 2004, 15:31:31 ; Search time 20 Seconds  
(without alignments)  
72.144 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_448\_462  
Perfect score: 83  
Sequence: 1 DSYLQDDPDSFQD 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2522

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%

## Listing first 45 summaries

Database : PIR 78;\*

- 1: Pir1;\*
- 2: Pir2;\*
- 3: Pir3;\*
- 4: Pir4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	33.7	12	PT0228	Ig heavy chain CDR
2	26	31.3	15	PS0185	27K protein A 3.4/
3	25	30.1	15	PO0195	sf11_glycoprotein
4	25	30.1	15	PO0193	styler_glycoprotei
5	24	28.9	12	SC0436	tachykinin - Afric
6	24	28.9	15	PO0194	sz-glycoprotein -
7	23	27.7	9	Ae0108	exotoxin A - Strept
8	21	25.3	5	SE8326	bilobal cell protein
9	21	25.3	10	S62880	polygalacturonase
10	21	25.3	11	SO7203	uperoxin - frog
11	21	25.3	11	PO7201	physalaemin - frog
12	21	25.3	14	PC079	unidentified 27.2K
13	21	25.3	15	PN0665	dystrophin-associated
14	21	25.3	15	PF0784	T-cell receptor al
15	20	24.1	7	B44787	calloseMRFamide 11
16	20	24.1	8	SL1078	Glucose-6-phosphate
17	20	24.1	11	BE0409	substance P-like pept
18	20	24.1	11	CG0409	kassinin-like pept
19	20	24.1	12	A55585	cytokinin-binding
20	20	24.1	12	CG0529	hemocyanin 1 - Gre
21	20	24.1	14	B38222	excinase ABC
22	20	24.1	15	150503	agrin - electric r
23	20	24.1	15	PF7789	gallbladder stone
24	19	22.9	6	PT0709	T-cell receptor be
25	19	22.9	9	PT0238	19 heavy chain CDR
26	19	22.9	10	GH01	gastric juice pept
27	19	22.9	10	AG1.07	sf11_glycoprotein -
28	19	22.9	10	JN0025	Persian tobacco (fragment)
29	19	22.9	11	BE0409	N; Alternate names: S1-glycoprotein

C;Species: Nicotiana alata (Persian tobacco)

## RESULT 1

PT0228

Ig heavy chain CDR3 region (clone 1-112) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C;Accession: PT0228

R; Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G. J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0228

A;Molecule type: DNA

A;Residues: 1-12 &lt;YAM&gt;

A;Experimental source: B lymphocyte

C;Keywords: heterotrimer; immunoglobulin

Query Match 33.7%; Score 28; DB 2; Length 12;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Query 4 YLQDSDPD 11

Db 1:1:1:

3 YVRDSSPE 10

## RESULT 2

PS0185

27K protein A 3.4/ rice (fragment)

C;Species: Oryza sativa (rice)

C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 24-Feb-1995

C;Accession: PS0185

R;Kamo, M.; Tauguita, A. Submitted to JIPID, June 1991

A;Reference number: PS0184

A;Accession: PS0185

A;Molecule type: protein

A;Residues: 1-15 &lt;KAM&gt;

Query Match 31.3%; Score 26; DB 2; Length 15;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Query 4 YLQDSDPD 12

Db 1:1:1:

4 YIVDVAPDS 12

## RESULT 3

PQ0195

Sf11\_glycoprotein - Persian tobacco (fragment)

N; Alternate names: S1-glycoprotein

C;Species: Nicotiana alata (Persian tobacco)

## ALIGNMENTS

C;Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 03-Aug-1998  
 C;Accession: PQ0195; PQ0173  
 R;Mau, S.L.; Atkinson, A.; Anderson, M.A.; Cornish, E.C.; Grego, B.; Simpson, R.;  
 Plantae 169, 184-191, 1986  
 A;Title: Style proteins of a wild tomato (*Lycopersicon peruvianum*) associated with expressio  
 A;Reference number: PQ0192  
 A;Accession: PQ0195  
 A;Molecule type: protein  
 A;Residues: 1-15 <MAU>  
 A;Experimental source: style  
 R;Jannen, W.; Butterham, M.P.; Clarke, A.E.; Moritz, R.L.; Simpson, R.  
 Plant Cell 1, 493-499, 1989  
 A;Title: Identification, isolation, and N-terminal sequencing of style glycoproteins ass  
 A;Reference number: PQ0173; MUID:92404717; PMID:2335548  
 A;Accession: PQ0173  
 A;Molecule type: protein  
 A;Residues: 1-15 <JAH>  
 A;Experimental source: style  
 C;Comment: This protein is involved in self-incompatibility of flowering plants.  
 C;Superfamily: Enterobacter ribonuclease  
 C;Keywords: Glycoprotein

Query Match 30.1%; Score 25; DB 2; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 5.9e+02;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYSYIQL 6  
 Db 1 DFBYIQL 6

RESULT 4  
 PQ0193  
 style glycoprotein 3 - Peruvian tomato (fragment)  
 N;Alternative names: S3-glycoprotein  
 C;Species: *Lycopersicon peruvianum* (Peruvian tomato)  
 C;Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 23-Aug-1997  
 C;Accession: A28133; A2819  
 R;Mau, S.L.; Williams, E.G.; Atkinson, A.; Anderson, M.A.; Cornish, E.C.; Grego, B.; Simpson, R.;  
 Plantae 169, 184-191, 1986  
 A;Title: Style proteins of a wild tomato (*Lycopersicon peruvianum*) associated with expressio  
 A;Reference number: PQ0192  
 A;Accession: PQ0193  
 A;Molecule type: protein  
 A;Residues: 1-15 <MAU>  
 A;Experimental source: style, strain Mill  
 R;Anderson, M.A.; Cornish, E.C.; Mau, S.L.; Williams, B.G.; Hoggart, R.; Atkinson, A.; E  
 J.P.; Crawford, R.J.; Clarke, A.E.  
 Nature 321, 39-44, 1986  
 A;Title: Cloning of cDNA for a stylar glycoprotein associated with expression of self-in  
 A;Reference number: A28819  
 A;Accession: A28819  
 A;Molecule type: protein  
 A;Residues: 1-15 <AND>  
 C;Keywords: Glycoprotein

Query Match 30.1%; Score 25; DB 2; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 5.9e+02;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYSYIQL 6  
 Db 1 DFDYIQL 6

RESULT 5  
 S07436  
 tachykinin - African tree frog (*Kassina maculata*)  
 N;Alternative names: hyalibatin  
 C;Species: *Kassina maculata*  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 02-Sep-2000  
 C;Accession: S07436

R;Yasuhara, T.; Nakajima, T.; Erspamer, G.F.; Erspamer, V.  
 Biomed. Res. 2, 613-617, 1981  
 A;Title: New tachykinins, Glu2, Pro5-kassinin (hyalibatin) and hyalibatin, in t  
 A;Reference number: S07436  
 A;Molecule type: protein  
 A;Residues: 1-12 <YAS>  
 A;Experimental source: skin  
 B;Note: the source is designated as *Hylambates maculatus*  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: amidated carboxyl end; neuropeptide; tachykinin  
 F;12/Modified site: amidated carboxyl end (Met) #status predicted  
 Query Match 28.9%; Score 24; DB 2; Length 12;  
 Best Local Similarity 80.0%; Pred. No. 6.7e-02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 9 DPDGF 13  
 |||||  
 Db 4 DPDGF 8

RESULT 6  
 PQ0194  
 S2-glycoprotein - Persian tobacco (fragment)  
 C;Species: *Nicotiana alata* (Persian tobacco)  
 C;Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 03-Mar-1995  
 C;Accession: PQ0194  
 R;Mau, S.L.; Williams, E.G.; Atkinson, A.; Anderson, M.A.; Cornish, E.C.; Grego, B.; Simpson, R.;  
 Plantae 169, 184-191, 1986  
 A;Title: Style proteins of a wild tomato (*Lycopersicon peruvianum*) associated with expressio  
 A;Reference number: PQ0192  
 A;Accession: PQ0194  
 A;Molecule type: protein  
 A;Residues: 1-15 <MAU>  
 A;Experimental source: style  
 C;Keywords: Glycoprotein

Query Match 28.9%; Score 24; DB 2; Length 15;  
 Best Local Similarity 46.2%; Pred. No. 8.6e+02;  
 Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DYSYLQSDPDGF 13  
 ||||| : |||||  
 Db 3 DMQLVLTXPASP 15

RESULT 7  
 A60108  
 exotoxin A - *Streptococcus pyogenes* (strain C203.S) (fragment)  
 N;Alternative names: blastogen A; scarlet fever toxin  
 C;Species: *Streptococcus pyogenes*  
 C;Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 07-Feb-1997  
 C;Accession: A60108  
 R;Achillevert, P.M.; Gray, E.D.  
 Infect. Immun. 57, 1865-1867, 1989  
 A;Title: Group A streptococcal pyrogenic exotoxin ('scarlet fever toxin) type A and blast  
 A;Reference number: A60108; MUID:89254013; PMID:2498210  
 A;Accession: A60108  
 A;Molecule type: protein  
 A;Residues: 1-9 <SCH>  
 C;Keywords: exotoxin

Query Match 27.7%; Score 23; DB 2; Length 9;  
 Best Local Similarity 80.0%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 QDSDP 10  
 |||||  
 Db 1 QDPDP 5

RESULT 8



Best Local Similarity 36.4%; Pred. No. 2.6e+03; Indels 0; Gaps 0;  
 Matches 4; Conservative 3; Mismatches 4;

Qy 2 YSYLQDSDPDS 12  
 Db 1 YTPLLDXXPNA 11

## RESULT 14

PH0784 T-cell receptor alpha chain (F1) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C;Accession: PH0784  
 R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
 J. Exp. Med. 174, 1371-1383, 1991  
 A;Title: T cell receptor genes in a series of class I major histocompatibility complex-  
 allele-exonuclease and antigen-specific repertoire.  
 A;Reference number: PH0746; PMID:92078846; PMID:1836010  
 A;Accession: PH0784  
 A;Molecule type: mRNA  
 A;Residues: 1-15 <CAS>  
 A;Cross-references: EMBL:X60885  
 A;Experimental source: T lymphocyte  
 C;Keywords: T-cell receptor

Query Match 25.3%; Score 21; DB 2; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 2.6e+03; Indels 0; Gaps 0;  
 Matches 3; Conservative 2; Mismatches 1;

Qy 8 SDDPSDF 13  
 Db 4 SDPSNY 9

## RESULT 15

B44787 calliphorafamide 11 - bluebottle fly (Calliphora vomitoria)  
 C;Species: Calliphora vomitoria  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 17-Mar-1999  
 C;Accession: B44787  
 R;Dure, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992  
 A;Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi  
 A;Reference number: A41978; PMID:9219611; PMID:1549595  
 A;Accession: B44787  
 A;Status: preliminary  
 A;Molecule type: Protein  
 A;Residues: 1-7 <DRV>  
 C;Keywords: amidated carboxyl end; neuropeptide F; 7/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 24.1%; Score 20; DB 2; Length 7;  
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 10 PDSF 13  
 Db 1 PDNF 4

Search completed: June 3, 2004, 15:35:16  
 Job time : 21 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: June 3, 2004, 15:27:56 ; Search time 11 Seconds  
(without alignments)  
71.005 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_448\_462  
Perfect score: 83  
Sequence: 1 DSYQLQSDPDSFQD 15

## Scoring table: BLOSUM62

Gapop 10.0 , Gapext: 0.5

## Searched:

141681 seqs, 52070155 residues

801

## Total number of hits satisfying chosen parameters:

Scored:

0

RESULT 1

TKN2\_KASMA  
ID TKN2\_KASMA  
AC P01614;  
DT 01-AUG-1998 (Rel. 08, Created)  
DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	24	28.9	12	1 TKN2_KASMA	P08614 kassina mac
2	23	27.7	10	1 CATB_SHEEP	P83305 ovis aries
3	23	27.7	13	1 GER1_HORVU	P28525 hordeum vul
4	23	27.7	13	1 GER2_HORVU	P28526 hordeum vul
5	23	27.7	15	1 EODA_LYMDI	P80338 lymantria d
6	22	26.5	11	1 TKN1_UPEIN	P82026 uperoleia i
7	21	25.3	11	1 TKN1_OPERU	P08612 uperoleia r
8	21	25.3	11	1 TKN1_PIXFU	P08615 physalaemus
9	20	24.1	7	1 FAR2_CALVO	P41666 calliphora
10	20	24.1	11	1 TKN2_PSEGU	P42387 pseudophryne
11	20	24.1	11	1 TKN2_UPERU	P08616 uperoleia r
12	20	24.1	11	1 TKN4_PSEGU	P42889 pseudophryne
13	20	24.1	12	1 HCY1_CARMA	P83176 carnius m
14	20	24.1	13	1 ECDE_LYMDI	P80941 lymantria d
15	20	24.1	13	1 LPAA_PORG1	P08611 porphyromon
16	19	22.9	10	1 GAJU_HUMAN	P01358 homo sapien
17	19	22.9	10	1 MOSQ_CLYJA	P19952 clupeaster
18	19	22.9	10	1 PPCK_FASHE	P8025 fasciola he
19	19	22.9	10	1 UHO5_RAT	P56573 rattus norvegicus
20	19	22.9	10	1 UPA9_HUMAN	P30095 homo sapien
21	19	22.9	11	1 TKN1_PSEGU	P42286 pseudophryne
22	19	22.9	12	1 TKN1_KASMA	P08613 kassina mac
23	19	22.9	14	1 GLGS_SPIOL	P55235 spinacia oleracea
24	18	21.7	8	1 AL16_CARMA	P81819 carnius m
25	18	21.7	8	1 PAR1_PANRE	P41872 panagrellus
26	18	21.7	9	1 NSKL_SARBU	P41192 sarcophaga
27	18	21.7	10	1 AMPN_HELAM	P81731 helicoverpa
28	18	21.7	10	1 LSK2_LEUMA	P09019 leucophaea
29	18	21.7	11	1 LSK1_LEUMA	P04228 leucophaea
30	18	21.7	11	1 LSKP_PERAM	P36385 periplaneta
31	18	21.7	11	1 TKN1_FANCA	P22688 ranaculus
32	18	21.7	12	1 LSK3_LOCMI	P47733 locusta mig
33	18	21.7	12	1 UTA1_MOUSE	P99032 mus musculus

## Description

CC -!- FUNCTION: Tachykinins are active peptides which excite neurons, evoke behavioral responses, are potent vasodilators and contract (directly or indirectly) many smooth muscles.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: skin.

CC -!- SIMILARITY: Belongs to the tachykinin family.

DR PIR; S07436; S07436

DR InterPro; IPR002040; Tachykinin.

DR Pfam; PF022020; Tachykinin; 1.

DR PROSITE; PS00267; TACHYKININ; 1.

DR Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.

FT MOD RES 12 12 AMIDATION.

SQ SEQUENCE 12 AA: 1441 MW: 3287CD2F0DD40AB7 CRC64;

Query Match Score 24; DB 1; Length 12;  
Best Local Similarity 80.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 DPDSF 13

Db 4 DPDRF 8

CATH\_SHEBP

STANDARD;

PRT; 10 AA.

ID CATH\_SHEBP

AC P83205;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Cathepsin B (EC 3.4.22.1) (Cathepsin B1) (Fragment).

DN Cathepsin B

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## ALIGNMENTS

RA Yasuhara T., Nakajima T., Ferspaner G.F., Brspaner V.;  
"New tachykinins, Glu2, Pro-kassinin (hyalambates-kassinin) and  
hyalambatin, in the skin of the African rhacophorid frog Hylambates  
maculatus".

RC Kassina maculata (African rhacophorid frog) (Hylambates maculatus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Kassina.  
OC NCBI\_TaxID=8414;

RN [1]

RP

RC TISSUE=Skin secretion;

RA "New tachykinins, Glu2, Pro-kassinin (hyalambates-kassinin) and  
hyalambatin, in the skin of the African rhacophorid frog Hylambates  
maculatus".

RC Biomed. Res. 2:613-617(1981).

CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
evolve behavioral responses, are potent vasoconstrictors (directly or indirectly) many smooth  
muscles.

CC -!- SUBCELLULAR LOCATION: Skin.

CC -!- TISSUE SPECIFICITY: Belongs to the tachykinin family.

DR PIR; S07436; S07436

DR InterPro; IPR002040; Tachykinin.

DR Pfam; PF022020; Tachykinin; 1.

DR PROSITE; PS00267; TACHYKININ; 1.

DR Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.

FT MOD RES 12 12 AMIDATION.

SQ SEQUENCE 12 AA: 1441 MW: 3287CD2F0DD40AB7 CRC64;

Query Match Score 24; DB 1; Length 12;

Best Local Similarity 80.0%; Pred. No. 3.4e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OC Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE;

RC TISSUE=Placenta;  
 RX MEDLINE=239405; PubMed=12500352;  
 RA El Amri B., Remey B., Souza N.M., Joris B., Ottiers N.G., Perenyi Z.,  
 RA Mboko H.B., Beckers J.-F.M.P.;  
 RT "Isolation and partial characterization of three pregnancy-associated  
 glycoproteins from the ewe placenta.";  
 RT Mol. Reprod. Dev. 64:199-206 (2003).  
 :- FUNCTION: Thiol protease which is believed to participate in  
 intracellular degradation and turnover of proteins. Has also been  
 implicated in tumor invasion and metastasis.

CC !- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity  
 for peptide bonds. Preferentially cleaves -Arg-Arg- $\text{Xaa}$  bonds in  
 small molecule substrates (thus differing from cathepsin L). In  
 addition to being an endopeptidase, shows peptidyl-dipeptidase  
 activity, liberating C-terminal dipeptides.

CC !- SUBUNIT: Dimer of a heavy chain and a light chain cross-linked  
 by a disulfide bond (By similarity).  
 CC !- SIMILARITY: Belongs to peptidase family Cl.

DR InterPro; IPR000169; SHPr07\_acsite.

DR PROSITE; PS000139; THIOL\_PROTEASE ASN; PARTIAL.

DR PROSITE; PS000640; THIOL\_PROTEASE CYS; PARTIAL.

DR PROSITE; PS000639; THIOL\_PROTEASE HIS; PARTIAL.

DR Hydrolase; Thiol protease; Lyosome.

FT 10 10  
 SEQUENCE 10 AA; 1177 MW; 8795780DDAA9D5BA CRC64;

Query Match 27.7%; Score 23; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PDSF 13  
 Db 2 DPSF 5

RESULT 3  
 GER1\_HORVU STANDARD; PRT; 13 AA.  
 AC P28525;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Germin GS1 (Fragment).  
 OS Hordeum vulgare (Barley).  
 OC Bukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poaceae; Pooidae;  
 OX Triticeae; Hordeum.  
 RN [1]

RP SEQUENCE;

RC STRAIN=cv. CM 72; TISSUE=Root;  
 RA Hurkman W.J., Tao H.P., Tanaka C.K.;  
 RT "Germin-like polypeptides increase in barley roots during salt  
 stress";  
 RT Plant Physiol. 97:366-374 (1991).

CC !- FUNCTION: May play a role in altering the properties of cell walls  
 during germinative growth.  
 CC !- SUBUNIT: Oligomer (believed to be a pentamer but probably hexamer)  
 (By similarity).

CC !- SUBCELLULAR LOCATION: SOLUBLE, MICROSONAL AND CELL WALL FRACTIONS.

CC !- TISSUE SPECIFICITY: Roots and coleoptile. In roots, present in  
 the mature region, but not in the tip. Not detected in leaves.

CC !- INDUCTION: Increased by salt stress in roots and decreased by salt  
 stress in coleoptile.

CC !- PTM: Glycosylation.

CC !- SIMILARITY: Belongs to the germin family.

DR InterPro; IPR001929; Germin.

DR PROSITE; PS00725; GERMIN; PARTIAL.

KW Apoplast; Cell wall; Glycoprotein; Multigene family.

FT UNSURE 10 10  
 FT NON\_TER 13 13  
 SEQUENCE 13 AA; 1484 MW; 43FB4A1AA3B7BD7 CRC64;

Query Match 27.7%; Score 23; DB 1; Length 13;  
 Best Local Similarity 57.1%; Pred. No. 5.4e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 DPDSDFD 15  
 Db 2 DPSPLQD 8

RESULT 5  
 ECDA\_LYMD1 STANDARD; PRT;  
 AC P8093;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Testis ecdisiotropin peptide A (mz).  
 OS Lymantria dispar (Gypsy moth).  
 OC Bukaryote; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Diptera; Glossata; Neoptera; Endopterygota; Lepidoptera; Noctuoidea;

DR InterPro; IPR001929; Germin.

DR PROSITE; PS00725; GERMIN; PARTIAL.

KW Apoplast; Cell wall; Glycoprotein; Multigene family.

FT UNSURE 10 10  
 FT NON\_TER 13 13  
 SEQUENCE 13 AA; 1484 MW; 43FB4A1AA3B7BD7 CRC64;

Query Match 27.7%; Score 23; DB 1; Length 13;  
 Best Local Similarity 57.1%; Pred. No. 5.4e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 DPDSDFD 15  
 Db 2 DPSPLQD 8

RESULT 4  
 GER2\_HORVU STANDARD; PRT;  
 AC P28526;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Germin GS2 (Fragment).  
 OS Hordeum vulgare (Barley).  
 OC Bukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OX Triticeae; Hordeum.  
 RN [1]

RP SEQUENCE;

RC STRAIN=cv. CM 72; TISSUE=Root;  
 RA Hurkman W.J., Tao H.P., Tanaka C.K.;  
 RT "Germin-like polypeptides increase in barley roots during salt  
 stress";  
 RT Plant Physiol. 97:366-374 (1991).

CC !- FUNCTION: May play a role in altering the properties of cell walls  
 during germinative growth.  
 CC !- SUBUNIT: Oligomer (believed to be a pentamer but probably hexamer)  
 (By similarity).

CC !- SUBCELLULAR LOCATION: SOLUBLE, MICROSONAL AND CELL WALL FRACTIONS.

CC !- TISSUE SPECIFICITY: Roots and coleoptile. In roots, present in  
 the mature region, but not in the tip. Not detected in leaves.

CC !- INDUCTION: Increased by salt stress in roots and decreased by salt  
 stress in coleoptile.

CC !- PTM: Glycosylation.

CC !- SIMILARITY: Belongs to the germin family.

DR InterPro; IPR001929; Germin.

DR PROSITE; PS00725; GERMIN; PARTIAL.

KW Apoplast; Cell wall; Glycoprotein; Multigene family.

FT UNSURE 10 10  
 FT NON\_TER 13 13  
 SEQUENCE 13 AA; 1484 MW; 43FB4A1AA3B7BD7 CRC64;

Query Match 27.7%; Score 23; DB 1; Length 13;  
 Best Local Similarity 57.1%; Pred. No. 5.4e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 DPDSDFD 15  
 Db 2 DPSPLQD 8

OC Lymantriidae; Lymantria.  
 RX NCBI\_TaxID=13123;  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=97387807; PubMed=9243792;  
 RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,  
 RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a  
 gonadotropin isolated from brains of Lymantria dispar pupae.";  
 RL Arch. Insect Biochem. Physiol. 36:37-49(1997).  
 CC -!- FUNCTION: Stimulates synthesis of ecdysteroid in the testes  
 of larvae and pupae.  
 SQ SEQUENCE 15 AA; 1712 MW; 12E8D8246B74EE26 CRC64;  
 Query Match 27.7%; Score 23; DB 1; Length 15;  
 Best Local Similarity 44.4%; Pred. No. 6.3e+02;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 DYSYLOSD 9  
 Db 7 EYEPLNDAD 15  
 Db 7 EYEPLNDAD 15

RESULT 6  
 ID \_TKN1\_UPEIN STANDARD; PRT; 11 AA.  
 AC P82026;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Uperoleia 1.1.  
 OS Uperoleia inundata (Floodplain toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC Myobatrachidae; Uperoleia.  
 RX [1] \_  
 RN  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin, secretion;  
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,  
 RA Adams G.W., Severini C.;  
 RT "Novel uperin peptides from the dorsal glands of the australian  
 floodplain toadlet Uperoleia inundata.";  
 RL Aust. J. Chem. 49:475-484(1996).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 evoke behavioral responses, are potent vasodilators and  
 secretagogues, and contract (directly or indirectly) many smooth  
 muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin, dorsal glands.  
 CC -!- MASS SPECTROMETRY: MW=1208; METHOD=FAB.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR InterPro; IPR00240; Tachykinin\_Neurokinin.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1226 MW; 3293633E59CDD457 CRC64;

Query Match 25.3%; Score 21; DB 1; Length 11;  
 Best Local Similarity 60.0%; Pred. No. 9.2e+02;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 DPDSF 13  
 Db 3 DPNNAF 7

RESULT 8  
 ID \_TKN\_PHYFU STANDARD; PRT; 11 AA.  
 AC P08615;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DB Physalaemin.  
 OS Physalaemus fuscumaculatus (Neotropical frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;  
 OC Leptodactylinae; Physalaemini.  
 RN  
 RP SEQUENCE.  
 RC TISSUE=Skin, secretion;  
 RX MEDLINE=66076612; PubMed=5657249;  
 RA Bergamini V., Anarsi A., Bertaccini G., Cei J.M.;  
 RT "Structure and pharmacological actions of physalaemin, the main  
 active polypeptide of the skin of Physalaemus fuscumaculatus.";  
 RL Experientia 20:489-490(1964).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 evoke behavioral responses, are potent vasodilators and  
 secretagogues, and contract (directly or indirectly) many smooth  
 muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.

QY 8 SDPDSF 13  
 Db 2 ADPNAF 7

RESULT 7  
 TKN1\_UPERU

CC -|- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; S07201; S07201; Tachykinin; Neurokinin.  
 DR InterPro; IPR002040; Tachykinin; Neurokinin.  
 DR Pfam; PF0202; Tachykinin; 1.  
 DR PS00167; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1 AMIDATION.  
 SQ SEQUENCE 11 AA; 1283 MW; 3293693E59033457 CRC64;

Query Match 25.3%; Score 21; DB 1; Length 11;  
 Best Local Similarity 50.0%; Pred. No. 9.2e+02;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 8 SDPDSF 13  
 :|:  
 Db 2 ADPNKEF 7

RESULT 9  
 FARB\_CALVO STANDARD; PRT; 7 AA.  
 ID P41866;  
 AC P41866;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Calliphoramide 11.  
 OS Calliphora vomitoria (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora.  
 OX NCBITaxID:27454;  
 RN [1] \_

RP SEQUENCE.  
 RC TISSUE-Thoracic ganglion;  
 RX MEDLINE=93196111; PubMed=15495955;  
 RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
 RA Rehfeld J.F., Thorpe A.;  
 RT "Isolation, structure, and activity of 'Phe-Met-Arg-Phe-NH2  
 neuropeptides (designated callifMRamides) from the blowfly  
 Calliphora vomitoria.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
 RL -|- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
 family.  
 DR PIR; B44787; B44787.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 7 7 AMIDATION.  
 SQ SEQUENCE 7 AA; 926 MW; 69DA0699C44AB700 CRC64;

Query Match 24.1%; Score 20; DB 1; Length 7;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 PDSF 13  
 :|:  
 Db 1 PDSF 4

RESULT 10  
 TKN2\_PSEGU STANDARD; PRT; 11 AA.  
 ID TKN2\_PSEGU  
 AC P42987;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Kassinin-like peptide K-II (PG-KII).  
 OS Pseudophryne guentheri (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC Myobatrachinae; Pseudophryne.  
 OX NCBITaxID:30349;  
 RN

SEQUENCE.  
 RP TISSUE=Skin secretion; PubMed=2356157;  
 RC MEDLINE=90287814; Published: 2000-01-01;  
 RX Simmaco M., Severini C., de Biase D., Barza D., Bossa F.,  
 RA Roberts J.D., Michiorri P.; Erspermer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 the Australian frog *Pseudophryne guntheri*."  
 RT Peptides 11:29-34 (1990).  
 RL -|- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC secretegous, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- TISSUE SPECIFICITY: Skin.  
 CC -|- SIMILARITY: Belongs to the tachykinin family.  
 CC -|- PIR: C60409; C60409;  
 DR InterPro; IPR002040; Tachykinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SMD0203; TKY; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 DR KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD RES 11 AA; 1246 MW; 3A247C379C81AB7 CRC64;  
 SQ SEQUENCE 11 AA; 1246 MW;  
 Query Match 24.1%; Score 20; DB 1; Length 11;  
 Best Local Similarity 60.0%; Pred. No. 1.3e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 9 DPDSF 13  
 DB 3 NPDEF 7

RESULT 11  
 TKN2\_UPERU STANDARD; PRT; 11 AA.  
 ID TKN2\_UPERU  
 AC P08616;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DB Rugesuperolein II ([Lys5,Thr6]physalaemin).  
 OS Uporelia rugosa (Wrinkled toadlet).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 CC Myobatrachinae; Uporelia.  
 RN [1] \_  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion; PubMed=73389029;  
 RX Nakajima T., Yasuhara T.; Erspermer G.F., Negri L.;  
 RT "Physalaemin- and bombesin-like peptides in the skin of the  
 Australian leptodactylid frog *Uporelia rugosa*."  
 RL Chem. Pharm. Bull. 28:659-659 (1980).  
 CC -|- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC secretegous, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- TISSUE SPECIFICITY: Skin.  
 CC -|- SIMILARITY: Belongs to the tachykinin family.  
 CC -|- PIR: IPR002040; Tachykinin.  
 DR InterPro; IPR002040; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 DR KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD RES 11 AA; 1270 MW;  
 SQ SEQUENCE 11 AA; 1270 MW;

Query Match Similarity 24.1%; Score 20; DB 1; Length 11;  
 Best Local Similarity 50.0%; Pred. No. 1.e+03; 2; Mismatches 1; Indels 0; Gaps 0;

CC -!- SEQUENCE. TISSUE:Hemolymph; PubMed=2620501;  
 CC MEDLINE=9015107; PIR: C60529; Neutelboom B., Sierdsema S.J., Beintema J.J.;  
 CC RA "The relationship of N-terminal sequences and immunological  
 CC characterization of crustacean hemocyanins.";  
 CC RL Comp. Biochem. Physiol. 94B:587-592(1989).  
 CC -!- FUNCTION: Hemocyanins are copper-containing oxygen carriers  
 CC occurring freely dissolved in the hemolymph of many mollusks and  
 CC arthropods.  
 CC -!- SUBCELLULAR LOCATION: Extracellular.  
 CC -!- TISSUE SPECIFICITY: Hemolymph.  
 CC -!- SIMILARITY: Belongs to the tyrosinase family. Hemocyanin  
 subfamily.

RESULT 12

TkN4\_PSEGU STANDARD; PRT; 11 AA.

Qy 8 SDPDSF 13  
 Db 2 ADPKCF 7

TKN4\_PSEGU STANDARD; PRT; 11 AA.

AC P42979; DT 01-NOV-1995 (Rel. 32, Created)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)

OS Substance P-like Peptide I (PG-SPI).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;

OC Myobatrachidae; Pseudophryne.

OX NCBI\_TaxID=30349; RN [1]

RP SEQUENCE.  
 RC TISSUE:Skin secretion; RX MEDLINE=028714; PubMed=2356157;

RA Siannaco M., Severini C.; de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Bruspaner V.; RT "Six novel tachykinin and bombesin-related peptides from the skin of  
 RT the Australian frog *Pseudophryne guntheri*.";  
 RL Peptides 11:29-30(1990).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.

DR PIR: E60499; E60409.  
 DR InterPro; IPR002040; Tachy Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam: PF02202; Tachykinin; SMART; SMART0203; RK; 1.  
 DR Pyrocidione carboxylic acid.

KW Pyrocidione carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD RES 1 1 AMIDATION.  
 SQ SEQUENCE 11 AA; 1294 MW; 3A2472CC9C81AB7 CRC64;

Query Match Similarity 24.1%; Score 20; DB 1; Length 11;  
 Best Local Similarity 60.0%; Pred. No. 1.3e+03; 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 SDPDSF 13  
 Db 3 NDEF 7

RESULT 13

Hcy1\_Carma STANDARD; PRT; 12 AA.

AC P83176; DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Hemocyanin subunit 1 (Fragment).

OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Bivalvia; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunoidea; Portunidae; Carcinus.

OX NCBI\_TaxID=6759; RN [1]

DE Lipid-A-associated protein (Fragment).  
OS Porphyromonas gingivalis (Bacteroides gingivalis).  
OC Bacteroidales; Bacteroidetes; Bacteroidales (class); Bacteroidales;  
OC Porphyromonadaceae; Porphyromonas.  
RN [1]  
RP NCBI\_TAXID=837;  
SEQUENCE  
STRAIN=950;  
RX MEDLINE:99061194; PubMed=9846737;  
RA Sharp L., Poole S., Reddi K., Fletcher J., Nair S., Wilson M.,  
RA Curtis M., Henderson B., Tabona P.;  
RT "A lipid A-associated protein of *Porphyromonas gingivalis*, derived  
RT from the hemaggulutinating domain of the RI protease gene family, is  
RT a potent stimulator of interleukin 6 synthesis.";  
RL Microbiology 144:3019-3026(1998).  
CC -!- FUNCTION: IS ASSOCIATED WITH LIPID A, A PHOSPHORYLATED GLYCOLIPID  
CC THAT ANCHORS THE LIPOPOLYSACCHARIDE TO THE OUTER MEMBRANE OF THE  
CC CELL.  
FT VARIANT 12 12 G -> F.  
FT NON\_TER 13 13  
FT SEQUENCE 13 AA; 1346 MW; 3BEA796EFAF63AB7 CRC64;  
Query Match 24.1%; Score 20; DB 1; Length 13;  
Best Local Similarity 40.0%; Pred. No. 1.6e+03;  
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
OY 6 QDSDPDSFQD 15  
| :|||  
Db 2 QGDNPDKDTD 11

Search completed: June 3, 2004, 15:33:51  
Job time : 11 secs

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OM protein - protein search, using sw model

Run on: June 3, 2004, 15:31:01 ; Search time 38 Seconds  
(without alignments)

124,547 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_448\_462

Perfect score: 83

Sequence: 1 DSYLQDDDDSFQD 15

Scoring table: BLOSUM62

Gapext 0.5

Searched: 1017041 seqs., 315518202 residues

Total number of hits satisfying chosen parameters: 3954

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SPTRNBL25:\*

- 1: sp\_archea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rrodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	25.5	30.7	15 4 Q9UCC4	Q9ubko homo sapien
2	22	26.5	15 6 Q9TR40	Q9346 homo sapien
3	25	30.1	15 10 Q9S8X0	Q9chz95 bos taurus
4	21	25.3	8 4 Q9HCQ0	Q93515 arabidopsis
5	22	26.5	8 12 Q9WUJ3	Q93562 nicotiana t
6	22	26.5	13 4 Q9UEE2	Q93563 mus musculus
7	22	26.5	13 4 Q9UEE3	Q93565 squash leaf
8	22	26.5	15 6 Q9TR40	Q93566 squash leaf
9	22	26.5	15 6 Q9TQQ9	Q93567 squash leaf
10	21	25.3	8 4 Q9HCQ0	Q93568 tobacco
11	21	25.3	9 4 Q9BYF9	Q93569 tobacco
12	21	25.3	11 2 P96319	Q93570 tobacco
13	21	25.3	12 6 Q9TQY4	Q93571 tobacco
14	21	25.3	13 2 Q9R7D6	Q93572 tobacco
15	21	25.3	13 12 Q9IBN1	Q93573 tobacco
16	21	25.3	14 12 Q84708	Q93574 tobacco

ALIGNMENTS			
<b>RESULT 1</b>			
ID Q9UCC4	PRELIMINARY;	PRT;	15 AA.
AC Q9UCC4;			
DT 01-MAY-2000 (TREMBLrel. 13, Created)			
DT 01-JUN-2000 (TREMBLrel. 13, Last sequence update)			
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)			
DB 33 kDa heparin-RELEASEABLE Protein (Fragment).			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
ON NCBI_TAXID=9606;			
RN [1]			
RP RPP			
RK MEDLINE:94059921; PubMed:8241100;			
RA Novotny W.F., Maffei T., Mata R.L., Milner P.G.;			
RT "Identification of novel heparin-releasable proteins, as well as the cytokines midkine and pleiotrophin, in human postheparin plasma.";			
RR Arterioscler. Thromb. 13:1798-1805 (1993).			
SQ SEQUENCE 15 AA; 1B23 MW: D5AF35664E7085D7 CRC64;			

SEQUENCE			
RPT			
Q9UCC4	PRELIMINARY;	PRT;	15 AA.
AC Q9UCC4;			
DT 01-MAY-2000 (TREMBLrel. 13, Created)			
DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)			
DB 33 kDa heparin-RELEASEABLE Protein (Fragment).			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
ON NCBI_TAXID=9606;			
RN [1]			
RP RPP			
RK MEDLINE:94059921; PubMed:8241100;			
RA Novotny W.F., Maffei T., Mata R.L., Milner P.G.;			
RT "Identification of novel heparin-releasable proteins, as well as the cytokines midkine and pleiotrophin, in human postheparin plasma.";			
RR Arterioscler. Thromb. 13:1798-1805 (1993).			
SQ SEQUENCE 15 AA; 1B23 MW: D5AF35664E7085D7 CRC64;			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SEQUENCE			
Best Local Similarity 33.3%			
Matches 5;	Conservative 4;	Mismatches 5;	Indels 1;
Score 30.7%;	DB 4;	Length 15;	Gaps 1;
SEQ			
RESULT 2			
Q9SSX0	PRELIMINARY;	PRT;	15 AA.
AC Q9SSX0;			
DT 01-MAY-2000 (TREMBLrel. 13, Created)			
DT 01-OCT-2003 (TREMBLrel. 13, Last sequence update)			
DB 1 DYSYVIFQADPQDYQ 14			
1 EYDYVIFQADPQDYQ 15			

Nicotiana alata (Winged tobacco) (Persian tobacco).

OC	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC	lamiids; Solanales; Solanaceae; Nicotiana.
OX	
NCBI_TAXID=4087;	
[1]	
SEQUENCE.	
MEDLINE=92404717;	PubMed=2535548;
RA	Jahnen W., Batterham M.P., Clarke A.B., Moritz R.L., Simpson R.J.;
RT	"Identificative, isolation, and N-terminal sequencing of stylet glycoproteins associated with self-incompatibility in Nicotiana alata." Plant Cell 1:493-499 (1989).
RT	PIR; PQ0195; PQ0195.
DR	GO; GO:0004521; F:endoribonuclease activity; IEA.
DR	GO; GO:003123; F:RNA binding; IEA.
DR	InterPro; IPR01568; RNase T2.
DR	Pfam; PF00445; ribonuclease_T2; 1.
SQ	SEQUENCE: 15 AA; 1829 MW; D9EDB655B262D66 CRC64;
Query Match	Score 25; DB 10; Length 15;
Best Local Similarity	66.7%; Pred. No. 1.6e+03;
Matches	4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy	1 DYSYIQL 6
Db	1 DFBYLQ 6
RESULT 3	
Q40563	PRELIMINARY; PRT; 15 AA.
ID	Q40563; (TREMBLrel. 01, Created)
AC	DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DB	DB Small_ras-related protein (Fragment).
GN	RAN-B2.
OS	Nicotiana tabacum (Common tobacco)
OC	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC	lamiids; Solanales; Solanaceae; Nicotiana.
OX	
NCBI_TAXID=4097;	
[1]	
SEQUENCE FROM N.A.	
STRAIN=SRL;	
RX	MEDLINE=98018947; PubMed=1987411;
RA	Merkle T., Haizel T., Matsumoto T., Harter K., Dallmann G., Nagy F.-.
RT	"Phenotype of the fission yeast cell cycle regulatory mutant pim1-46 is suppressed by a tobacco cDNA encoding a small, Ran-like GTP-binding protein".
RT	Plant J. 6: 555-565 (1994).
RL	EMBL; L16788; AXA73656; 1; -.
DR	GO:0005225; F:GTP binding; IEA.
KW	GTP-binding.
FT	NON_TER
SQ	SEQUENCE: 15 AA; 1604 MW; 9A57F48FLFFPFPAF CRC64;
Query Match	Score 25; DB 10; Length 15;
Best Local Similarity	40.0%; Pred. No. 1.6e+03;
Matches	4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy	5 LQPSDPDSQ 14
Db	6 LPDDDEAFE 15
RESULT 4	
Q14342	PRELIMINARY; PRT; 14 AA.
ID	Q14342; (TREMBLrel. 01, Created)
AC	DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT	DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
FLII	ERGB transcription factor (F-fragment).
GN	FLII.
OS	Homo sapiens (Human).
DB	FYN protein (Fragment).
GN	Homo sapiens (Human).
CC	Kawakami T., Kawakami Y., Aaronson S.A., Robbins K.C.;
CC	"Acquisition of transforming properties by FYN, a normal SRC-related human gene." Proc. Natl. Acad. Sci. U.S.A. 85:3870-3874 (1988).
OX	[1] _TAXID=9606;
RN	SEQUENCE FROM N.A.
RX	MEDLINE=88234523; PubMed=3287380;
RA	Kawakami T., Kawakami Y., Aaronson S.A., Robbins K.C.;
RT	"Acquisition of transforming properties by FYN, a normal SRC-related human gene." Proc. Natl. Acad. Sci. U.S.A. 85:3870-3874 (1988).
RL	[1] _TAXID=9606;
DR	EMLBL; M20285; AAA52492.1; -.
FT	NON_TER
SQ	SEQUENCE: 14 AA; 1825 MW; 4F3CBDD2E572BA17 CRC64;
Query Match	Score 24; DB 4; Length 14;
Best Local Similarity	54.5%; Pred. No. 2.2e+03;
Matches	6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy	4 YLQDSDPDSQ 14
Db	2 YLQSFLDYFQ 12
RESULT 5	
Q9WUJ3	PRELIMINARY; PRT; 8 AA.
ID	Q9WUJ3; (TREMBLrel. 12, Created)
AC	DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT	DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DT	DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DB	DB Suid herpesvirus 1 putative UL47 and UL46 genes and partial gB (Fragment).
GN	GB.
GS	Pseudorabies virus (strain Kaplan) (PRV).
GS	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC	Alphaherpesvirinae; Varicellovirus.
RN	SEQUENCING FROM N.A.
RP	SEQUENCING FROM N.A.
RA	Bras F., Dezelies S., Simonet B., Nguyen X., Vende P., Flamand A., Masse M.-J.; (TREMBLrel. 1, Last sequence update)
RA	RA "The left border of the genomic inversion of pseudorabies virus contains genes homologous to the UL46 and UL47 genes of Herpes Simplex Virus type 1, but no UL45 gene."
RA	Virus Res. 60:29-40 (1999).
RA	EMBL; AJ010303; CAA09075.1; -.
FT	NON_TER
SQ	SEQUENCE: 8 AA; 875 MW; 262DDAB76AA05BB CRC64;
Query Match	Score 22; DB 12; Length 8;
Best Local Similarity	42.9%; Pred. No. 1e+06;
Matches	3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy	6 QDSDPDS 12
Db	1 ESEDPPDA 7
RESULT 6	
Q9UEE2	PRELIMINARY; PRT; 13 AA.
ID	Q9UEE2; (TREMBLrel. 13, Created)
AC	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE	DE ERGB transcription factor (F-fragment).
GN	FLII.
OS	Homo sapiens (Human).



RL Eur. J. Biochem. 267:5943-5951 (2000).  
DR EMBL; AB017179; BAB16368..1; -.  
DR GO; GO:0041112; F:cyclic-nucleotide phosphodiesterase activity; NAS.  
ST Sequence 8 AA; 96 MW; FD4B19D5A6C76446 CRC64;  
SQ

Query Match Score 21; DB 4; Length 8;  
Best Local Similarity 42.9%; Pred. No. 1e+06;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 DPDSEFD 15  
Db 2 NPQSPEN 8

RESULT 11

Q9BYF9 PRELIMINARY; PRT; 9 AA.  
ID Q9BYF9; PRELIMINARY; PRT; 9 AA.  
AC AC; Q9BYF9; PRELIMINARY; PRT; 9 AA.  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Cytokeratin 19 (Fragment).  
GN K19.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
OC Mammalia; Butheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1] SEQUENCE FROM N.A.; PubMed=11682035;  
RP  
RA Kagaya M., Kaneko S., Ohno H., Inamura K., Kobayashi K.;  
RT "Cloning and characterization of the 5'-flanking region of human  
cytokeratin 19 gene in human cholangiocarcinoma cell line.";  
RL Hepatol. 35:504-511(2001).  
DR EMBL; AB05973; BAB0770..1; -.  
DR GO; GO:0005882; C:intermediate filament; IEA.  
KW Keratin.  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 1122 MW; 9E9FC41B45AB45A1 CRC64;

Query Match Score 21; DB 4; Length 9;  
Best Local Similarity 80.0%; Pred. No. 1e+06;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YSYLQ 6  
Db 4 YSYRQ 8

RESULT 12

P96319 PRELIMINARY; PRT; 11 AA.  
ID P96319; PRELIMINARY; PRT; 11 AA.  
AC AC; P96319; PRELIMINARY; PRT; 11 AA.  
DT 01-MAY-1997 (TREMBLrel. 03, Created)  
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE Coded portion of proteobacterial protein tag (Fragment).  
OS Desulfovibrio desulfuricans.  
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;  
OC Desulfovibrionaceae; Desulfovibrio.  
OX NCBI\_TaxID=876;  
RN [1] SEQUENCE FROM N.A.; STRAIN=ATCC 27774;  
RC STRAIN=ATCC 27774; PubMed=8972778;  
RX MEDLINE=97128184; PubMed=8972778;  
RA Williams K.P., Bartels D.P.;  
RT "Phylogenetic analysis of tmRNA secondary structure.";  
RL RNA 2..130..131(1995).  
DR EMBL; U68081; ARAB4803..1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1250 MW; 85776D58CBSABB5A CRC64;

Query Match Score 21; DB 2; Length 11;  
Best Local Similarity 75.0%; Pred. No. 5.4e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSY 4  
Db 6 DYAY 9

RESULT 13

Q9RYQ4 PRELIMINARY; PRT; 12 AA.  
ID Q9RYQ4; PRELIMINARY; PRT; 12 AA.  
AC AC; Q9RYQ4; PRELIMINARY; PRT; 12 AA.  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Glycoprotein H-B N-TERMINAL, GPH-B N-TERMINAL-KEX2/subtilisin-related  
protein (Fragment).  
OS Bos taurus (Bovine).  
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
OC Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
OC Bovidae; Bovinae; Bos.  
RN [1];  
RN SEQUENCE;  
RP MEDLINE=91340701; PubMed=1874725;  
RA Christie D.L., Batchelor D.C., Palmer D.J.;  
RT "Identification of hex2-related proteases in chromaffin granules by  
partial amino acid sequence analysis.";  
RL J. Biol. Chem. 266:15679-15683 (1991).  
FT NON\_TER 12  
SQ SEQUENCE 12 AA; 1303 MW; 9P2FF9E78782DC5BA CRC64;  
PRT; 13 AA.

Query Match Score 21; DB 6; Length 12;  
Best Local Similarity 54.5%; Pred. No. 5.9e+03;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 SYLQDSDPSF 13  
Db 1 SVLXDSALDF 11

RESULT 14

Q9RD66 PRELIMINARY; PRT; 13 AA.  
ID Q9RD66; PRELIMINARY; PRT; 13 AA.  
AC AC; Q9RD66; PRELIMINARY; PRT; 13 AA.  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
RN [1];  
RN SEQUENCE FROM N.A.; STRAIN=damanna;  
RA Yang G.H.;  
RT toxin;"  
RL Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.  
RN Clostridium botulinum.  
OS Clostridium botulinum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1491;  
RN [1];  
RN SEQUENCE FROM N.A.; STRAIN=damanna;  
RA "Nontoxic components of Clostridium botulinum type B progenitor  
toxin.";  
RL Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.  
RN Clostridium botulinum.  
OS Clostridium botulinum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1491;  
RN [1];  
RN SEQUENCE 13 AA; 1552 MW; 98356108PA6FD041 CRC64;

Query Match Score 21; DB 2; Length 13;  
Best Local Similarity 57.1%; Pred. No. 6.5e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YSYLQD 8  
Db 1 :| :|

Db 4 YSTIONS 10

RESULT 15

Q9IEN1	PRELIMINARY;	PRT;	13 AA.
ID Q9IEN1;			
AC Q9IEN1;			
DT 01-OCT-2000	(TREMBLeL 15, Created)		
DT 01-OCT-2000	(TREMBLeL 15, Last sequence update)		
DE Influenza A/mayo clinic/103/74 (H1N1), non-structural protein (Seg 8), cooh terminus of ns1 (Fragment).			
DE Influenza A virus (strain A/Mayo clinic/103/74).			
OS Viruses; ssRNA negative strand viruses; Orthomyxoviridae;			
OC Influenza A viruses; Influenza A.			
OC NCBITaxID=11437;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=a/mayo clinic/103/74;			
RX MEDLINE=83303830; PubMed=6612993;			
RA Parvin J.D., Young J.F., Palese P.;			
RT "nonsense mutations affecting the lengths of the ns1 nonstructural proteins of influenza a virus isolates.";			
RT Virology 128:512-517 (1983).			
DR EMBL; K00960; AAA3523.2; -.			
FT NON_TER 1			
FT NON_TER 13			
SQ SEQUENCE	13 AA; 1673 MW;	51550D3C579F56D7 CRC64;	
Query Match	25.3%;	Score 21;	DB 12;
Best Local Similarity	57.1%;	Pred. No. 6.5e+03;	Length 13;
Matches 4;	Conservative 1;	Mismatches 2;	Indels 0;
QY 1 DYSTIQD 7			Gaps 0;
	:		
Db 2 DLAYLQN 8			

Search completed: June 3, 2004, 15:34:43  
Job time : 39 secs

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OM protein - protein search, using SW model

Run on: June 3, 2004, 17:03:29 ; Search time 53 Seconds (without alignments)

Scoring table: BLOSUM62 Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

- 1: geneseqP1980s:\*
- 2: geneseqP1990s:\*
- 3: geneseqP2000s:\*
- 4: geneseqP2001s:\*
- 5: geneseqP2002s:\*
- 6: geneseqP2003as:\*
- 7: geneseqP2003bs:\*
- 8: geneseqP2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	83	100.0	15	2	AAW15323	Aaw15323 Class II
2	83	100.0	15	2	AAJ33169	Aay33169 Human tyr
3	83	100.0	15	2	AAU00711	Aay00711 Tumour an
4	83	100.0	15	2	AAV49659	Aay49659 Tumour an
5	83	100.0	15	2	AAV01749	Aay01749 Exemplary
6	83	100.0	15	3	AAV71516	Aay71516 Human Tyr
7	83	100.0	15	3	AAV90800	Aay90800 Human leu
8	83	100.0	15	3	AAV23672	Aab23672 Cytotoxic
9	83	100.0	15	3	AAV92296	Aay92296 Tyrosinas
10	83	100.0	15	3	AAV156611	Aay156611 Tyrosinas
11	83	100.0	15	3	AAV84292	Aay84292 Tumour as
12	83	100.0	15	3	AAV82975	Aay82975 Tyrosinas
13	83	100.0	15	3	AAB02618	Aab02618 Tumour as
14	83	100.0	15	3	AAV08690	Aab08690 Antigenic
15	83	100.0	15	4	AAE02107	Aae02107 Tyrosinas
16	83	100.0	15	4	AAE1350	Aab1350 Exemplary
17	83	100.0	15	4	AAE06837	Aae06837 Human tyr
18	83	100.0	15	5	ABG79140	Abg79140 Human tyr
19	83	100.0	15	6	ADA19544	Ada19544 Human can
20	79	95.2	15	2	AAV15354	Aaw15354 Class II
21	79	95.2	15	2	AAW15331	Aaw15331 Class II
22	79	95.2	15	2	AAW15332	Aaw15332 Class II
23	77	92.8	14	2	AAW15324	Aaw15324 Class II
24	77	92.8	15	2	AAW15353	Aaw15353 Class II
25	75	90.4	15	2	AAW15330	Aaw15330 Class II
26	75	90.4	15	2	AAW15333	Aaw15333 Class II
27	74	89.2	15	2	AAW15334	Aaw15334 Class II
28	74	89.2	15	2	AAW15325	Aaw15325 Class II
29	70	84.3	13	2	AAW15326	Aaw15326 Class II
30	70	84.3	13	2	AAY40210	Aay40210 Amino aci
31	70	84.3	13	2	AAY26856	Aay26856 Melanoma
32	70	84.3	13	3	AAB1740	Peptide F
33	70	84.3	13	3	ABG79141	Human Tyr
34	70	84.3	13	5	AAE19079	HIF-1 <sup>+</sup> DP4 r
35	66	79.5	12	2	AAW15355	Aaw15355 Class II
36	61	73.5	13	2	AAC017104	Tyrosinas
37	59	71.1	11	2	AAW15356	Aaw15356 Class II
38	58	69.9	12	2	AAW15352	Aaw15352 Class II
39	34	41.0	9	6	ABR17773	Human can
40	34	41.0	9	6	ABR17403	Human can
41	34	41.0	9	6	ABR18233	Human can
42	34	41.0	9	6	ABR17639	Human can
43	34	41.0	9	6	ABR17977	Human can
44	34	41.0	10	6	ABR18156	Human can
45	34	41.0	10	6	ABR18149	Human can

## ALIGNMENTS

RESULT 1	
ID	AAW15323
XX	AAW15323 standard; peptide; 15 AA.
AC	AAW15323;
XX	DE 09-FEB-1998 (first entry)
XX	Class II restricted melanoma tyrosinase derived antigenic peptide
XX	DE Major histocompatibility complex; MHC; Class II; tyrosinase; vaccine; immune response; immunogenic peptide; melanoma treatment; protective antibody; immune cells; CD8+ T cell; CD4+ T cell.
XX	XX Synthetic.
OS	OS Homo sapiens.
XX	BN WO9711669-A2.
XX	DD 03-APR-1997.
XX	DD 25-SEP-1996; 96WO-US015346.
XX	DD 26-SEP-1995; 95US-00533895.
PA	(USSH ) US DEPT HEALTH & HUMAN SERVICES.
PI	Topalian SL, Rosenberg SA, Robbins PF;
XX	DR WPI; 1997-212652/19.
FT	Major histocompatibility complex Class II immunogenic peptide - used to prevent or treat melanoma in mammal by stimulating production of protective antibodies or immune cells.
FS	Claim 2: Page 59: 79pp; English.
CC	Peptides AAW15321-56 are major histocompatibility complex (MHC) Class II restricted melanoma peptides, derived from tyrosinase. Tumour reactive human CD4+ and CD8+ T cells recognise melanoma antigens encoded by the tyrosinase gene. The present sequence is derived from amino acids 48-462. The peptides may be used as a vaccine, either prophylactically in advance of any evidence of melanoma, or therapeutically to enhance the patient's own immune response. The immunogenic peptides can be used to prevent or treat melanoma in a mammal by stimulating the production of protective antibodies or immune cells, preferably immune positive CD4+ T cells.

RESULT 2  
Y33169 AAY33169 standard; peptide; 15 AA.

17-NOV-1999 (first entry)  
Human tyrosinase peptide #8.  
Human; protein delivery; Yersinia *Br*  
immune response; cytotoxic T-lympho-  
pathological disorder; tyrosinase.

*omo sapiens.*

WO945198-A2.  
 10-SEP-1999.  
 03-MAR-1999; 99WO-IB000587.  
 06-MAR-1998; 98WO-00036582.  
 (VBRG/) VAN DER BRUGGEN P B.  
 (CORN/) CORNELIS G R.  
 (EOLA/) ROLAND A M.  
 (BOON/) BOON-FALLEUR T R.  
 Van Der Bruggen PB, Cornelis G  
 WEI; 1999-540840/45.

New mutant *Yersinia* strains useful for treating a pathological disorder.

This invention describes a novel mutant *Yersinia* (Y1) strain, comprising immunogen(s) in effector-encoding gene(s) and deficient in the production of functional effector protein(s). The invention describes (1) a quintuple mutant *Yersinia* strain, having the designation *Yersinia enterocolitica* YOPHOMP or *Yersinia pseudotuberculosis* YOPPHAO; (2) an expression vector (YEV1) for delivering in the 5' - 3' direction; (3) a *Yersinia* or *Yersinia* strain for delivering a heterologous protein into a eukaryotic cell, comprising contacting the cell with a Y1 transformed expression vector (YEV1) with the above vector (Y1-EV1); (4) a method for delivering a heterologous protein into a eukaryotic cell, comprising contacting the cell with a Y1 transformed with the above vector (Y1-EV1); (5) a method for inducing an immune response specific for a heterologous protein; (6) a method for inducing a cytotoxic T-lymphocyte (CTL) response specific for a heterologous protein; (7) a method for determining the efficacy of an antigen vaccination regimen in a subject. Y1 is used to treat a pathological disorder, by providing recombinant *Yersinia* for the safe delivery of proteins into eukaryotic cells. *YAY33147-Y3319* are human-derived peptides used to illustrate the method of the invention.



PN	WO200032769-A2.	PI	Ooms A,	De Giovanni G,	Morel S,	Van Den Eynde B,	Boon-Falleur T;
XX	08-JUN-2000.	XX	XX	XX	XX	XX	WPI; 2000-11784/27.
XX	PF 26-NOV-1999;	PR	Isolated peptides, sometimes derived from tyrosinase, which bind to HLA-B35 leading to recognition and lysis of the resulting complexes by cytolytic T cells.	XX	XX	XX	
XX	27-NOV-1998;	PR		XX	XX	XX	
XX	PA (LUDW-) LUDWIG INST CANCER RES.	PS	Example 3; Page 9; 20pp; English.	XX	XX	XX	
XX	PI Huang L, Van Pei A, Brasseur F, De Plaen E, Boon T;	CC	The present invention describes isolated peptides which bind to human leukocyte antigen (HLA)-B35 molecules leading to recognition and lysis of the resulting complexes by cytolytic T cells. The isolated peptides are sometimes derived from tyrosinase. Compositions comprising the peptides of the invention can be used to generate immune responses in humans, but also in non-human animals to generate immune components which can then be used to treat humans or diagnostically.	CC	CC	CC	
XX	DR Novel polypeptides expressed in tumor cells useful for treating cancer have an ability to complex with a major histocompatibility complex molecule and comprises a specific unbroken amino acid sequence.	CC	Therapeutically, the peptides are useful in generation of cytolytic T cells either in vitro or in vivo which specifically lyse pathogenic cells. The peptides can also be used to identify HLA-B35 positive cells, or to remove HLA-B25 positive cells from mixtures containing such cells.	CC	CC	CC	
XX	PT Disclosure; Page 19; BOPP; English.	CC	Nucleic acid molecules encoding the peptides can be used inter alia as probes to identify cells which are expressing tyrosinase. The present sequence represents an HLA binding peptide used in the exemplification of the present invention	CC	CC	CC	
XX	PS Sequence 15 AA;	CC	Sequence 15 AA;	CC	CC	CC	
XX	XX	Query Match Score 83; DB 3; Length 15;	Query Match Score 83; DB 3; Length 15;	XX	XX	XX	
XX	XX	Best Local Similarity 100.0%; Pred. No. 1.7e-06;	Best Local Similarity 100.0%; Pred. No. 1.7e-06;	XX	XX	XX	
XX	XX	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	XX	XX	
XX	XX	Qy 1 DYSYIQLQDSDPDSFQD 15	Qy 1 DYSYIQLQDSDPDSFQD 15	XX	XX	XX	
XX	XX	Db 1 DYSYIQLQDSDPDSFQD 15	Db 1 DYSYIQLQDSDPDSFQD 15	XX	XX	XX	
XX	XX	Sequence 15 AA;	Sequence 15 AA;	XX	XX	XX	
XX	XX	RESULT 8	RESULT 8	XX	XX	XX	
XX	XX	AAB23672	AAB23672 standard; peptide; 15 AA.	XX	XX	XX	
XX	XX	ID AAB23672	ID AAB23672 standard; peptide; 15 AA.	XX	XX	XX	
XX	XX	AC AAB23672;	AC AAB23672;	XX	XX	XX	
XX	XX	DT 05-JAN-2001 (first entry)	DT 05-JAN-2001 (first entry)	XX	XX	XX	
XX	XX	DE Cytotoxic T lymphocyte (CTL) epitope SEQ ID NO:24.	DE Cytotoxic T lymphocyte (CTL) epitope SEQ ID NO:24.	XX	XX	XX	
XX	XX	KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL; immune response; infectious disease; malaria; cytotoxic T cell; cytostatic; immunomodulant; cellular immune response inducer; protozoaide; leukaemia; cancer.	KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL; immune response; infectious disease; malaria; cytotoxic T cell; cytostatic; immunomodulant; cellular immune response inducer; protozoaide; leukaemia; cancer.	XX	XX	XX	
XX	XX	OS Homo sapiens.	OS Homo sapiens.	XX	XX	XX	
XX	XX	PN WO200049041-A1.	PN WO200049041-A1.	XX	XX	XX	
XX	XX	PI Shinbara N, Udonoh H, Yui K;	PI Shinbara N, Udonoh H, Yui K;	XX	XX	XX	
XX	XX	PD 20-APR-2000.	PD 20-APR-2000.	XX	XX	XX	
XX	XX	PP 04-OCT-1999;	PP 04-OCT-1999;	XX	XX	XX	
XX	XX	99WO-US023038.	99US-00169717.	XX	XX	XX	
XX	XX	PA (LUDW-) LUDWIG INST CANCER RES.	PA (LUDW-) LUDWIG INST CANCER RES.	XX	XX	XX	
XX	XX	PS Claim 7; Page 57; 72pp; Japanese.	PS Claim 7; Page 57; 72pp; Japanese.	XX	XX	XX	

XX The present invention describes a fused protein (I) prepared from a peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by cytotoxic T cells and a protein containing the ATPase domain of a heat shock protein. Also described are: (1) a drug composition containing (I) as active ingredient; (2) a DNA encoding (I); (3) an expression vector containing the DNA of (2); and (4) a transformant which can retain the expression vector of (3). (I) has cytotoxic, immunostimulant and protozoacide activities, and can be used as a cellular immune response inducer. The protein is useful as an active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer e.g. to provide systemic immunity against leukaemia. The present sequence represents a specifically claimed CTL epitope for use in a fused protein of the present invention.

XX Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

RESULT 9

AAY92296  
ID AAY92296 standard; peptide; 15 AA.  
XX AAY92296;

DT 10-AUG-2000 (first entry)

DE Tyrosinase antigenic peptide epitope (residues 448-462).  
XX Tyrosinase; antigen; epitope; cytotoxic T lymphocyte; CTL; complex;  
KW human leukocyte antigen; HLA.  
XX OS Homo sapiens.  
XX PN WO2000020445-A2.  
XX PD 13-APR-2000.

XX PF 15-SEP-1999; 99WO-IB001664.  
XX PR 02-OCT-1998; 98US-00165863.  
PR 09-APR-1999; 99US-00289350.  
XX PA (CHAU/) CHAUX P.  
PA (LIUTT/) LIUTTEN R.  
PA (DEM0/) DEMOTE N.  
PA (DUFF/) DUFFOUR M.  
PA (LURQ/) LURQUIN C.  
PA (TRAV/) TRAVERSARI C.  
PA (STRO/) STROOBANT V.  
PA (CORN/) CORNELIS G.R.  
PA (BOON/) BOON-PALLEUR T.  
PA (VBRU/) VAN DER BRUGGEN P.  
PA (SCHU/) SCHUITZ E.  
PA (WARN/) WARNIER G.

XX Chaux P, Luitjen R, Demotte N, Duffour M, Lurquin C, Traversari C, Stroobant V, Cornelis GR, Boon-Palleur T, Van Der Bruggen P;  
PI PI Schultz E, Warnier G;  
XX DR WPI; 2000-303739/26.

PT Isolation of cytotoxic T-lymphocytes clones by successive steps of stimulation and testing of lymphocytes with antigen presenting cells which present antigens derived from different expression systems.

XX Disclosure; Page 22; 99pp; English.

XX A novel method of isolation of cytotoxic T-lymphocytes (CTL) clones comprises successive steps of stimulation and testing of lymphocytes with antigen presenting cells (APCs) which present antigens derived from different expression systems. The CTL clones is isolated recognize specific antigenic peptides of proteins. Preferably the APC is autologous and each expression systems is different from at least one of the other expression systems, therefore isolating a cytotoxic T cell clone specific for the protein. The method can also be used to identify an antigenic peptide epitope. Isolated CTL clones specific for a peptide/human leukocyte antigen (HLA) complex are claimed. The CTL cells specific for the complexes, peptides or cells which present the complexes on the cell surface are useful for treating pathological conditions characterized by abnormal expression of the complexes

PS Disclosure; Page 22; 99pp; English.

XX A novel method of isolation of cytotoxic T-lymphocytes (CTL) clones comprises successive steps of stimulation and testing of lymphocytes with antigen presenting cells (APCs) which present antigens derived from different expression systems. The CTL clones is isolated recognize specific antigenic peptides of proteins. Preferably the APC is autologous and each expression systems is different from at least one of the other expression systems, therefore isolating a cytotoxic T cell clone specific for the protein. The method can also be used to identify an antigenic peptide epitope. Isolated CTL clones specific for a peptide/human leukocyte antigen (HLA) complex are claimed. The CTL cells specific for the complexes, peptides or cells which present the complexes on the cell surface are useful for treating pathological conditions characterized by abnormal expression of the complexes

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;

Query Match 100.0%; Score 83; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1 DSYLQSDPDSFQD 15  
Db 1 DSYLQSDPDSFQD 15

PS Sequence 15 AA;



CC	acids 448-462 of the tyrosinase polypeptide. See also AAY82953-Y82986	
XX	Sequence 15 AA;	
SQ	Score 100.0%; DB 3; Length 15;	
Query Match	Best Local Similarity 100.0%; Pred. No. 1.7e-06;	
Best Local Similarity 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Matches 15;		
Db	1 DYSYIQLQSDPDPDFQD 15	1 DYSYIQLQSDPDPDFQD 15
Db	1 DYSYIQLQSDPDPDFQD 15	1 DYSYIQLQSDPDPDFQD 15
RESULT 13		
AAB02618	ID AAB02618 standard; peptide; 15 AA.	
XX		
AC	AAB02618;	
XX		
DT	18-AUG-2000 (first entry)	
XX		
DE	Tumour associated peptide antigen from Tyrosinase #7.	
XX		
KW	MAGE-A3; HLA class II; human leukocyte antigen; antibody; vaccine;	
KW	cancer; human; tumour; tumour associated gene product.	
OS	Homo sapiens.	
XX		
XX		
PR	WO2000020581-A1.	
XX		
PN		
PD	13-APR-2000.	
XX		
PF	15-SEP-1999; 99WO-US021230.	
XX		
PR	05-OCT-1998; 99US-00166448.	
XX		
PA	(LUDW-) LUDWIG INST CANCER RES.	
PA	(UYVR-) UNIV VRIJE BRUSSEL.	
XX		
PI	Schultz P, Stroobant V, Boon-Falleur T, Van Der Bruggen P, Corthals J, Heirman C;	
PI	Chaux P, Van Snick J, Lethe B, Thielemans K,	
DR	WPI; 2000-31713/27.	
XX		
PT	New MAGE-A3 class II binding peptides, useful to diagnose and treat tumors, are fragments of MAGE-A3 which bind to and are presented to T lymphocytes by human leukocyte antigen class II molecules.	
PT	The present invention relates to MAGE-A3 (tumour associated gene product) human leukocyte antigen (HLA) class II-binding peptides (see AAB02566-B02595, and AAB02633-B02637). These Peptides are presented to T cells in the context of HLA class II molecules. The Peptides stimulate the activity and proliferation of CD4+ T lymphocytes. The invention also includes nucleotide sequences encoding MAGE-3A peptides (see AAA37928 and AAA37941-A37942).	
CC	The present invention relates to MAGE-A3 (tumour associated gene product) human leukocyte antigen (HLA) class II-binding peptides, the antibodies, peptides and nucleotide sequences can be used to create a vaccine. The peptides are used to diagnose or treat a disorder characterized by expression of MAGE-3, particularly cancer. The methods can also be used in the diagnosis of disorders associated with MAGE-3 expression. Included in the invention are other human tumour antigens (see AAB02596-02637), and PCR primers used in the course of the invention (see AAA37929-A37937 and AAA37941-A37942).	
CC	Sequence 15 AA;	
XX		
Query Match	Best Local Similarity 100.0%; Pred. No. 1.7e-06;	100.0%; Score 83; DB 3; Length 15;
Best Local Similarity 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 15;		
Db	1 DYSYIQLQSDPDPDFQD 15	1 DYSYIQLQSDPDPDFQD 15
Db	1 DYSYIQLQSDPDPDFQD 15	1 DYSYIQLQSDPDPDFQD 15
RESULT 15		
AAB02107	ID AAB02107 standard; peptide; 15 AA.	
XX		
AC	AAB02107;	
XX		
DT	31-JUL-2001 (first entry)	
XX		

DE Tyrosinase human leukocyte antigen-DR4-binding peptide #2.  
 XX Human; cytostatic; immunogen; Tyrosinase; human leukocyte antigen; HLA;  
 KW CD8; cytotoxic T lymphocyte; cancer; carcinoma; melanoma; myeloma;  
 KW brain tumour; sarcoma; vaccine; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200078806-A1.  
 PD 28-DEC-2000.  
 XX  
 PF 14-JUN-2000; 2000WO-US016297.  
 XX  
 PR 18-JUN-1999; 99US-00336091.  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Van Snick J, Leche B, Chaux P, Boon-Falleur T, Van Der Bruggen P;  
 XX DR WPI; 2001-102698/11.  
 XX  
 PT Novel MAGE-A1 human leukocyte antigen class II peptides which bind to and  
 PT are presented to the class II molecules, useful for inducing immune  
 PT response and treating cancers characterized by expression of MAGE-A1.  
 XX  
 PS Disclosure: Page 33; 78pp; English.  
 XX  
 CC AAB31302-59 represent exemplary antigens which are characteristic of  
 CC tumours. They can be used to enhance the immune response of vaccines  
 CC comprising peptides derived from human MAGE-A1 HLA (human leukocyte  
 CC antigen) class I-binding protein. Peptides derived from the MAGE-A1 HLA  
 CC binding protein stimulate the activity and proliferation of CD4+ T  
 CC lymphocytes. The MAGE-A1 HLA binding protein is useful as a diagnostic  
 CC agent for diagnosing a disorder characterized by expression of MAGE-A1.  
 CC The protein is used for treating a disorder characterized by expression  
 CC of MAGE-A1 such as cancers e.g. melanoma, squamous cell carcinomas,  
 CC colorectal carcinomas, osteosarcomas, and lymphocytic leukemias. Peptides  
 CC derived from the MAGE-A1 HLA binding protein are useful in the production  
 CC of anti-tumour vaccines  
 XX  
 SQ Sequence 15 AA:  
 Query Match 100.0%; Score 83; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYSYLQDSDPSFQD 15  
 DB 1 DYSYLQDSDPSFQD 15

RESULT 17  
 AAB06837 standard; peptide; 15 AA:  
 XX  
 AC AAB06837;  
 XX  
 DT 16-OCT-2001 (first entry)

XX  
 DE Human tyrosinase antigenic peptide #7.  
 XX  
 AC AAB06837;  
 XX  
 DT 16-OCT-2001 (first entry)  
 XX  
 DE Human tyrosinase antigenic peptide #7.  
 XX  
 AC AAB06837;  
 XX  
 DT 16-OCT-2001 (first entry)  
 XX  
 DE Human tyrosinase antigenic peptide #7.  
 XX  
 AC AAB06837;  
 XX  
 DT 16-OCT-2001 (first entry)  
 XX  
 DE Human tyrosinase antigenic peptide #7.

XX  
 DE MAGE antigenic peptide; Human leukocyte antigen; HLA-B35; HLA-B44;  
 KW tumour cell; immunostimulant; antigen presentation; cancer; melanoma;  
 KW CD8+ cytotoxic T lymphocyte; colorectal; prostate; Gastric carcinoma;  
 KW myeloma; brain tumour; sarcoma; seminoma; ovarian tumour; cycostatic;  
 KW gene therapy; tumour rejection antigen; TRA; human; tyrosinase; MHC;  
 KW major histocompatibility complex.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200153033-A1.  
 PD 26-JUL-2001.  
 XX  
 PR 19-JAN-2001; 2001WO-US002008.  
 XX  
 PR 20-JAN-2000; 2000US-0177243B.  
 KW  
 DE Exemplary antigen characteristic of tumours, derived from tyrosinase.  
 XX  
 KW MAGE-A1; HLA; human leukocyte antigen; CD4+ T lymphocyte; cancer;  
 KW MAGE-A1 HLA class I-binding protein; vaccine.

PR 25-OCT-2000; 2000US-0243212P.  
 PA (LUDWIG) LUDWIG INST CANCER RES.  
 XX  
 PI Luitjen R, Boon-Falleur T, Van Der Bruggen P, Stroobant V;  
 PI Demotte N, Schultz E;  
 XX  
 DR WPI; 2001-488724/53.

PT Functional variants and isolated mimetics of a MAGE-A1 HLA-B35 or HLA-B44 binding peptide, or of a MAGE-A3 HLA-B35 binding peptide, used in PT diagnosis and treatment of a disorder characterized by expression of MAGE PT -A1 or -A3.

PS Disclosure: Page 28; 103PP; English.

The invention relates to functional variants and isolated mimetics of a MAGE-A1 human leukocyte antigen (HLA)-B35 or HLA-B44 binding peptide, or of a MAGE-A3 HLA-B35 binding peptide, identified by methods described in the specification. MAGE genes encode tumour rejection antigens (TRAs) presented to T lymphocytes by HLA-B35 and HLA-B44 molecules. The MAGE antigenic peptide acts by binding to HLA molecules on tumour cells and stimulating recognition of these cells and thus signalling them to the immune system for destruction. The peptide when presented by HLA molecule induces the activation and stimulation of CD8+ cytotoxic T lymphocytes. The MAGE antigenic peptide is used to treat and diagnose disorders characterised by expression of MAGE-A1 or -A3. Disorders include cancers e.g. melanomas, oesophageal, lung, head and neck, breast, colorectal, prostate, renal, bladder, hepatocellular, papillary thyroid and gastric carcinomas, myelomas, brain tumours, sarcomas, seminomas, and ovarian tumours. The present sequence is human tyrosinase tumour associated antigenic peptide presented by major histocompatibility complex (MHC) HLA -D4. The antigenic peptide is used in combination with peptides of the invention for inducing an immune response.

SQ Sequence 15 AA;

Query Match 100.0%; Score 83; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQDSDPSDFQD 15  
 1 DYSYLQDSDPSDFQD 15

Db 1 DYSYLQDSDPSDFQD 15

RESULT 18  
 ABG/9140

ID ABG79140 standard; peptide; 15 AA.

XX

AC ABG79140;

XX DT 15-NOV-2002 (first entry)

DE Human Tyrosinase class II HLA tumour-restricted antigen peptide #2.

KW Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen; KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia; KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer; KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer; ovarian cancer; pancreatic cancer; vaccine; dendritic cell; KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA; KW cycostatic; human.

OS Homo sapiens.

XX PN WO200264057-A2.

XX PD 22-AUG-2002.

XX PP 15-FEB-2002; 2002WO-US005212.

XX PR 15-FEB-2001; 2001US-0268687P.

XX (BAYU ) BAYLOR COLLEGE MEDICINE.

PA XX

PI XX

DR XX

WPI; 2002-627577/67.

XX

Novel composition for treating a disease in an animal, comprises an PR immune effector cell and cell penetrating peptide associated with an PR antigen or antibody.

XX Disclosure: Page 22; 61PP; English.

PS XX

The invention relates to a composition (I) comprising an immune effector cell and a cell penetrating peptide (CPP) associated with an antigen or antibody. Also included are (1) a vaccine comprising (I), CPP associated with an antigen, and a pharmaceutically acceptable carrier and (2) preparing a composition for a disease, by providing (I) and CPP associated with an antigen for disease, and introducing the antigen-associated CPP to (1), where antigen enters into the cell. The antigens are, for example, tumour antigen derived epitopes recognised by tumour infiltrating lymphocytes (TILs) of HLA (human leukocyte antigen) class I or II. The composition is useful for enhancing immunity in an animal to a disease, by administering a mature dendritic cell comprising CPP associated with an antigen to disease, to the animal, such that following the administration, animal is protected from disease, where the animal comprises both CD4+ and CD8+ T cells. It is also useful for treating a disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung cancer, non-Hodgkin's lymphoma, Hodgkin's lymphoma, uterine cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma, breast cancer, prostate cancer, ovarian cancer and pancreatic cancer). The animal is further subjected to a cancer treatment including surgery, radiation, chemotherapy or gene therapy. The administration of (I), preferably dendritic cell is prior to, subsequent to or concurrent with, the cancer treatment. The present sequence is a tumour antigen derived epitope for inclusion in the composition of the invention.

XX Sequence 15 AA;

Query Match 100.0%; Score 83; DB 5; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYSYLQDSDPSDFQD 15

Db 1 DYSYLQDSDPSDFQD 15

RESULT 19

ABD19544

ADA19544 standard; peptide; 15 AA.

XX

AC ADA19544;

XX DT 20-NOV-2003 (first entry)

DE Human cancer antigen, tyrosinase (MHC HLA-DR4) #2.

KW Lymphoid tissue-specific cell; haematoopoietic progenitor cell; KW lymphoreticular stromal cell; transplantation; implantation; KW autoimmune disease; infectious disease; maintenance; expansion; KW therapeutic; differentiated progeny; antigen; MHC; KW major histocompatibility complex; cancer; human.

OS Homo sapiens.

XX PN US6548299-B1.

XX PD 15-APR-2003.

XX PP 18-MAY-2000; 2000US-00574749.

XX PR

22-AUG-2002.

XX PN WO200264057-A2.

XX PR 15-FEB-2002; 2002WO-US005212.

XX PR 15-FEB-2001; 2001US-0268687P.

12-NOV-1999; 99R0-US026795.  
Pykett M J. Rosenzweig M. Scadden D T. Poznansky M C. Pykett MJ, Rosenzweig M, So WPT: 2003-60374/57

Inducing lymphoid tissue-specific cell *in vivo*, useful in diseases by transplantation, implantation, autoimmune and/or infectious diseases by producing hematopoietic progenitor and lymphoreticular stromal cells , a porous solid matrix.

closure; SEQ ID NO 25; 34pp; English;

The invention discloses a method for producing lymphoid tissue-specific cell in vivo, comprising introducing haematopoietic progenitor cells and lymphoreticular stromal cells into a porous, solid matrix having interconnected pores of a pore size sufficient to permit the cells to grow throughout the matrix, and co-culturing the haematopoietic progenitor cells and lymphoreticular stromal cells. The methods are useful in transplantation, implantation, autoimmune diseases and/or infectious diseases. They are particularly useful for *in vivo* maintenance, expansion and/or differentiation of haematopoietic progenitor cells, for inducing T cell tolerance, for treating a subject to enhance immune tolerance, for inducing T-cell reactivity, and for identifying an agent suspected of affecting haematopoietic cell development. The lymphoid tissue-specific cells are useful in laboratory analysis and in therapeutics. The method provides rapid generation of a large number of differentiated progeny. The sequence presented is a cancer antigen which was used in the invention to expand haematopoietic progenitor cells.

כט עזרא

Query Match Score 83; DB 6; Length 15;  
 Best Local Similarity Pred. No. 1.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels

1 DYSYLQDSDPDSFQD 15  
1 DYSYLQDSDPDSFQD 15  
1 DYSYLQDSDPDSFQD 15

search completed: June 3, 2004, 17:04:38  
Search time: 55 seconds

Copyright GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model

Run on: June 3, 2004, 15:34:47 ; Search time 42 Seconds (without alignments)

1000.478 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_448\_462

Perfect score: 83

Sequence: 1 DSYLQDSDPDSFQD 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 199639

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Published Applications AA:  
 1: /cgnd\_6/picodata/1/pubpaas/US07\_PUBCCMB.pep:  
 2: /cgnd\_6/picodata/1/pubpaas/PCT\_NEW\_PUB.pep:  
 3: /cgnd\_6/prodata/1/pubpaas/US06\_NEW\_PUB.pep:  
 4: /cgnd\_6/prodata/1/pubpaas/US07\_NEW\_PUB.pep:  
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 9: /cgnd\_6/prodata/1/pubpaas/US09A\_PUBCOMB.pep:  
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 11: /cgnd\_6/prodata/1/pubpaas/US09C\_PUBCOMB.pep:  
 12: /cgnd\_6/prodata/1/pubpaas/US09\_NEW\_PUB.pep:  
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 15: /cgnd\_6/prodata/1/pubpaas/US10C\_PUBCOMB.pep:  
 16: /cgnd\_6/prodata/1/pubpaas/US10C\_PUBCOMB.pep:  
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 18: /cgnd\_6/prodata/1/pubpaas/US60\_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	15	9	US-09-923-831-26
2	83	100.0	15	9	US-09-766-889A-18
3	83	100.0	15	12	US-10-218-95-33
4	83	100.0	15	14	US-10-161-97-25
5	83	100.0	15	14	US-10-170-832-67
6	70	84.3	13	9	US-09-847-185-42
7	70	84.3	13	14	US-10-224-286-42
8	70	84.3	13	15	US-10-406-317-14
9	70	84.3	13	16	US-10-676-90-30
10	70	84.3	13	16	US-10-297-168-14
11	34	41.0	14	12	US-10-103-395-72
12	33	39.8	10	9	US-09-962-05-22
13	33	39.8	10	9	US-09-976-740-22
14	33	39.8	10	12	US-10-671-242-22
15	33	39.8	10	13	US-10-023-529-22

**ALIGNMENTS**

```

RESULT 1
US-09-923-831-26
; Sequence 26, Application US/09923831
; Patent No. US2000115142A1
; GENERAL INFORMATION:
;   APPLICANT: Marselange, Val, rie
;   APPLICANT: De Smet, Charles
;   APPLICANT: Boon-Falleur, Thierry
;   TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
;   FILE REFERENCE: L0461/7054
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 09/183,706
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 43
; SEQ ID NO 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-831-26

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Query Match 100.0%; Score 83; DB 9; Length 15;

Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSYLQDSDPDSFQD 15

Dy 1 DSYLQDSDPDSFQD 15

**RESULT 2**  
US-09-766-889A-18  
; Sequence 38, Application US/09766889A  
; Patent No. US200216654A1  
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre

APPLICANT: Stroobant, Vincent  
 APPLICANT: Demotte, Nathalie  
 APPLICANT: Schultz, Erwin  
 TITLE OF INVENTION: IMAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44  
 FILE REFERENCE: LO461/7104  
 CURRENT APPLICATION NUMBER: US/09/766, 889A  
 PRIORITY APPLICATION NUMBER: US/09/766, 889A  
 CURRENT FILING DATE: 2001-01-19  
 PRIORITY APPLICATION NUMBER: US/09/177, 242  
 PRIOR FILING DATE: 2000-01-20  
 PRIORITY APPLICATION NUMBER: 2000-10-25  
 PRIORITY FILING DATE: 2000-10-25  
 NUMBER OF SEQ ID NOS: 59  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 38  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-766-889A-38

Query Match 100.0%; Score 83; DB 9; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSYLQDSDPDSFQD 15  
 Db 1 DSYLQDSDPDSFQD 15

RESULT 3  
 US-10-218-095-33  
 Sequence 33, Application US/10218095  
 Publication No. US2004003354-A1  
 GENERAL INFORMATION:  
 APPLICANT: Zhang, Yi  
 APPLICANT: Stroobant, Vincent  
 APPLICANT: Russo, Vincenzo  
 APPLICANT: Boon-Falleur, Thierry  
 APPLICANT: van der Bruggen, Pierre  
 TITLE OF INVENTION: MAGE-A4 ANTIGENIC PEPTIDES AND USES THEREOF  
 FILE REFERENCE: LO461/70137  
 CURRENT APPLICATION NUMBER: US/10/218, 095  
 CURRENT FILING DATE: 2002-08-13  
 NUMBER OF SEQ ID NOS: 63  
 SOFTWARE: Patentin version 3.1  
 SEQ ID NO: 33  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-218-095-33

Query Match 100.0%; Score 83; DB 12; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4  
 US-10-161-097-25  
 Sequence 25, Application US/10161097  
 Publication No. US2003009640-A1  
 GENERAL INFORMATION:  
 APPLICANT: ROSENZWEIG, Michael  
 APPLICANT: PYKETT, Mark J.  
 APPLICANT: SCADDEN, David T.  
 APPLICANT: POZNANSKY, Mark C.  
 TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION  
 TITLE OF INVENTION: HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL  
 FILE REFERENCE: CL005/7012-KA/ERG  
 CURRENT APPLICATION NUMBER: US/10/161, 097

Query Match 100.0%; Score 83; DB 14; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSYLQDSDPDSFQD 15  
 Db 1 DSYLQDSDPDSFQD 15

RESULT 5  
 US-10-170-832-67  
 Sequence 67, Application US/10170832  
 Publication No. US2003017092-A1  
 GENERAL INFORMATION:  
 APPLICANT: Chaux, Pascal  
 APPLICANT: Vancome, Valrie  
 APPLICANT: Stroobant, Vincent  
 APPLICANT: Boon-Falleur, Thierry  
 APPLICANT: van der Bruggen, Pierre  
 APPLICANT: Thielmans, Kris  
 APPLICANT: Corrhaas, Jurgen  
 TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
 FILE REFERENCE: LO461/7052  
 CURRENT APPLICATION NUMBER: US/10/170, 892  
 PRIOR APPLICATION NUMBER: US/09/166, 448  
 PRIOR FILING DATE: 1998-10-05  
 NUMBER OF SEQ ID NOS: 81  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 67  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-170-832-67

Query Match 100.0%; Score 83; DB 14; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSYLQDSDPDSFQD 15  
 Db 1 DSYLQDSDPDSFQD 15

RESULT 6  
 US-09-847-185-42  
 Sequence 42, Application US/09847185  
 Patent No. US20030076392-A1  
 GENERAL INFORMATION:  
 APPLICANT: SSO HOO, William  
 TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
 COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNO-  
 RESPONSE USING SAME  
 NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CAMPBELL & FLORES, LLP  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: United States  
 ZIP: 92121

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/847,185  
 FILING DATE: 01-May-2001  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 09/201,931  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-IM 2442  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)535-8901  
 TELEFAX: (619)535-8949  
 INFORMATION FOR SEQ ID NO: 42:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 42:  
 US-09-847-185-42

RESULT 7  
 US-10-224-286-42  
 / Sequence 42, Application US/10244286  
 / Publication No. US20030108517A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Soo Hoo, William  
 / TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
 / COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
 / RESPONSE USING SAME  
 / NUMBER OF SEQUENCES: 50  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: CAMPBELL & FLORES, LLP  
 / STREET: 4370 La Jolla Village Drive, Suite 700  
 / CITY: San Diego  
 / STATE: California  
 / COUNTRY: United States  
 / ZIP: 92121

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/224,286  
 FILING DATE: 19-Aug-2002  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US/08/902,516  
 FILING DATE: 29-JUL-1997

; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-IM 2442  
; TELEPHONE: (619)535-8901  
; TELEFAX: (619)535-8949  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 42:  
; US-10-224-286-42

Query Match      84.3%; Score 70; DB 14; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.00032;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 SYLQDSDPDSFQD 15  
 Db      1 SYLQDSDPDSFQD 13

RESULT 8  
 US-10-406-317-14  
 / Sequence 14, Application US/10406317  
 / Publication No. US20040019195A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Schlom, Jeffrey;  
 / APPLICANT: Hodge, James;  
 / APPLICANT: Panicl, Dennis  
 / TITLE OF INVENTION: A recombinant vector expressing multiple constitutatory  
 / genes of invention; molecules and uses thereof  
 / FILE REFERENCE: 38163-0189  
 / CURRENT APPLICATION NUMBER: US/10/406,317  
 / CURRENT FILING DATE: 2003-04-04  
 / PRIORITY APPLICATION NUMBER: US/09/856,988  
 / PRIORITY FILING DATE: 2001-05-30  
 / PRIORITY APPLICATION NUMBER: PCT/US99/26866  
 / PRIORITY FILING DATE: 1999-11-12  
 / PRIORITY APPLICATION NUMBER: 60/111,582  
 / PRIORITY FILING DATE: 1998-12-09  
 / NUMBER OF SEQ ID NOS: 41  
 / SOFTWARE: PatentIn Ver. 2.1  
 / SEQ ID NO: 14  
 / LENGTH: 13  
 / TYPE: PRT  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC  
 / OTHER INFORMATION: Peptide  
 / US-10-406-317-14

Query Match      84.3%; Score 70; DB 15; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.00032;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 SYLQDSDPDSFQD 15  
 Db      1 SYLQDSDPDSFQD 13

RESULT 9  
 US-10-676-909-30  
 / Sequence 30, Application US/10676909  
 / Publication No. US20040086521A1  
 / GENERAL INFORMATION:  
 / APPLICANT: KROPHOFER, H.  
 / APPLICANT: VOGT, A.  
 / TITLE OF INVENTION: Method for the identification of antigenic peptides associated to  
 / diseases

FILE REFERENCE: 21388  
; CURRENT APPLICATION NUMBER: US/10/676,909  
; CURRENT FILING DATE: 2003-10-01  
; PRIOR APPLICATION NUMBER: EP 02022223.8  
; PRIOR FILING DATE: 2002-02-10  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 30  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Homo sapiens

Query Match 84.3%; Score 70; DB 16; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.00032; Mismatches 0; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYLQDSDPDSFQD 15  
Db 1 SYLQDSDPDSFQD 13

RESULT 10  
US-10-297-168-14  
Sequence 14, Application US/10297168  
Publication No. US2004009195A1  
GENERAL INFORMATION:  
APPLICANT: SCHIOM, Jeffrey  
ATTORNEY/AGENT INFORMATION:  
APPLICANT: GREINER, John W.  
APPLICANT: KASS, Erik  
APPLICANT: PANICALI, Dennis  
TITLE OF INVENTION: RECOMBINANT NON-REPLICATING VIRUS EXPRESSING GM-CSF AND TITLE OF INVENTION: USES THEREOF TO ENHANCE IMMUNE RESPONSES  
FILE REFERENCE: 38163-0167  
CURRENT APPLICATION NUMBER: US/10/297,168  
CURRENT FILING DATE: 2002-12-03  
PRIOR APPLICATION NUMBER: PCT/US01/19201  
PRIOR FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: US60/211,717  
PRIOR FILING DATE: 2000-06-15  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 14  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Homo sapiens

Query Match 84.3%; Score 70; DB 16; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.00032; Mismatches 0; Indels 0; Gaps 0;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SYLQDSDPDSFQD 15  
Db 1 SYLQDSDPDSFQD 13

RESULT 11  
US-10-103-395-72  
Sequence 72, Application US/1010395  
Publication No. US20020160019A1  
GENERAL INFORMATION:  
APPLICANT: EPIMMUNE, Inc.  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR FILE REFERENCE: 39643-2016-01  
CURRENT APPLICATION NUMBER: US/10/103,395  
CURRENT FILING DATE: 2003-01-03  
PRIOR APPLICATION NUMBER: US 09/009,953  
PRIOR FILING DATE: 1998-01-21

PRIOR APPLICATION NUMBER: PCT/US98/01373  
; PRIOR FILING DATE: 1998-01-23  
; PRIOR APPLICATION NUMBER: US 60/036,713  
; PRIOR FILING DATE: 1997-01-23  
; PRIOR APPLICATION NUMBER: US 60/037,432  
; PRIOR FILING DATE: 1997-02-07  
; NUMBER OF SEQ ID NOS: 274  
; SOFTWARE: FastSeq For Windows Version 4.0  
; SEQ ID NO: 72  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-103-395-72

Query Match 41.0%; Score 34; DB 12; Length 14;  
Best Local Similarity 63.6%; Pred. No. 1.1e+02; Mismatches 4; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 LDQSDPDSFQD 15  
Db 4 LTGIPDSFQD 14

RESULT 12  
US-09-962-055-22  
Sequence 22, Application US/09962055  
Patent No. US2002005033A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Robert S.  
Lees, Ann M.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATOR SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/962,055  
FILING DATE: 24-Sep-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/979,608  
FILING DATE: 26-Nov-1997  
APPLICATION NUMBER: US 60/031,930  
FILING DATE: 27-Nov-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3963/5981B)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
SEQUENCE: Sidney, John  
SEQUENCE LENGTH: 10 amino acids  
SEQUENCE TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
US-09-962-055-22

Query Match 39.8%; Score 33; DB 9; Length 10;

Best Local Similarity 62.5%; Pred. No. 1.1e+02; Mismatches 2; Indels 0; Gaps 0; SEQ ID NO: 53  
 Matches 5; Conservative 1; Software: FastSEQ for Windows Version 4.0

Qy 6 QDSDPDSF 13  
 Db 1 EDDDPDGF 8

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RESULT 13  
 US-09-976-740-22  
 Sequence 22, Application US/09976740  
 Publication No. US20020194633A1  
 GENERAL INFORMATION:  
 APPLICANT: Lees, Ann M.  
 APPLICANT: Lees, Robert S.  
 APPLICANT: Arjona, Anibal A.  
 APPLICANT: Law, Simon W.  
 TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING ATHEROSCLEROSIS

FILE REFERENCE: 10797-004001  
 CURRENT APPLICATION NUMBER: US/09/976,740  
 CURRENT FILING DATE: 2001-10-12  
 PRIOR APPLICATION NUMBER: 09/616,289  
 PRIOR FILING DATE: 2000-07-14  
 PRIOR APPLICATION NUMBER: US 08/979,608  
 PRIOR FILING DATE: 1997-11-26  
 PRIOR APPLICATION NUMBER: US 60/031,930  
 PRIOR FILING DATE: 1996-11-27  
 PRIOR APPLICATION NUMBER: US 60/048,547  
 PRIOR FILING DATE: 1997-06-03  
 NUMBER OF SEQ ID NOS: 53  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 22  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-976-740-22

Query Match 39.8%; Score 33; DB 9; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 1.1e+02; Mismatches 2; Indels 0; Gaps 0; SEQ ID NO: 53  
 Matches 5; Conservative 1; Software: FastSEQ for Windows Version 4.0  
 Software: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 22  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-671-242-22

RESULT 14  
 US-10-671-242-22  
 Sequence 22, Application US/10671242  
 Publication No. US20040040045A1  
 GENERAL INFORMATION:  
 APPLICANT: Lees, Ann M.  
 APPLICANT: Lees, Robert S.  
 APPLICANT: Arjona, Anibal A.  
 APPLICANT: Law, Simon W.  
 TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING ATHEROSCLEROSIS

FILE REFERENCE: 10797-004001  
 CURRENT APPLICATION NUMBER: US/10/671,242  
 CURRENT FILING DATE: 2003-09-24  
 PRIOR APPLICATION NUMBER: US/09/616,289  
 PRIOR FILING DATE: 2000-07-14  
 PRIOR APPLICATION NUMBER: US 09/517,849  
 PRIOR FILING DATE: 2000-03-02  
 PRIOR APPLICATION NUMBER: US 08/979,608  
 PRIOR FILING DATE: 1997-11-26  
 PRIOR APPLICATION NUMBER: US 60/031,930  
 PRIOR FILING DATE: 1996-11-27  
 PRIOR APPLICATION NUMBER: US 60/048,547  
 PRIOR FILING DATE: 1997-06-03  
 NUMBER OF SEQ ID NOS: 53  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 22  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-023-529-22

RESULT 15  
 US-10-023-529-22  
 Sequence 22, Application US/10023529  
 Publication No. US20020129368A1  
 GENERAL INFORMATION:  
 APPLICANT: Lees, Ann M.  
 APPLICANT: Lees, Robert S.  
 APPLICANT: Law, Simon W.  
 APPLICANT: Arjona, Anibal A.  
 TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING ATHEROSCLEROSIS

CURRENT APPLICATION NUMBER: US/10/023,529  
 CURRENT FILING DATE: 2001-12-17  
 PRIOR APPLICATION NUMBER: 09/616,289  
 PRIOR FILING DATE: 2000-07-14  
 PRIOR APPLICATION NUMBER: US 09/517,849  
 PRIOR FILING DATE: 2000-03-02  
 PRIOR APPLICATION NUMBER: US 08/979,608  
 PRIOR FILING DATE: 1997-11-26  
 PRIOR APPLICATION NUMBER: US 60/031,930  
 PRIOR FILING DATE: 1996-11-27  
 PRIOR APPLICATION NUMBER: US 60/048,547  
 PRIOR FILING DATE: 1997-06-03  
 NUMBER OF SEQ ID NOS: 53  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 22  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-023-529-22

Query Match 39.8%; Score 33; DB 13; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 1.1e+02; Mismatches 2; Indels 0; Gaps 0; SEQ ID NO: 53  
 Matches 5; Conservative 1; Software: FastSEQ for Windows Version 4.0  
 Software: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 22  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-023-529-22

Search completed: June 3, 2004, 15:40:20  
 Job time : 42 secs

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## OM protein - protein search, using sw model

Run on: June 3, 2004, 15:32:26 ; Search time 23 Seconds

(without alignments)  
33.669 Million cell updates/sec

Title: US-08-533-895A-39\_COPY\_448\_462

Perfect score: 83

Sequence: 1 DYSYLOQSDPDSFQD 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

146418

Minimum DB seq length: 0  
Maximum DB seq length: 15Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing First 45 Summaries

Database :

Issued Patents AA:  
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 3: /cgm2\_6\_ptodata/2/iaa/5N\_COMB.pep:  
 4: /cgm2\_6\_ptodata/2/iaa/6B\_COMB.pep:  
 5: /cgm2\_6\_ptodata/2/iaa/PCTUS\_COMB.pep:  
 6: /cgm2\_6\_ptodata/2/iaa/backfile1.pep:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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2	83	100.0	15	3 US-09-183-706-26 Sequence 26, Appl
3	83	100.0	15	4 US-09-166-448-67 Sequence 67, Appl
4	83	100.0	15	4 US-09-567-995-26 Sequence 26, Appl
5	83	100.0	15	4 US-09-165-863-23 Sequence 23, Appl
6	83	100.0	15	4 US-09-697-984-67 Sequence 67, Appl
7	83	100.0	15	4 US-09-289-350-23 Sequence 23, Appl
8	83	100.0	15	4 US-09-574-749B-25 Sequence 25, Appl
9	83	100.0	15	4 US-09-318-141-23 Sequence 23, Appl
10	83	100.0	15	4 US-09-169-717E-29 Sequence 29, Appl
11	70	84.3	13	2 US-08-902-516-42 Sequence 23, Appl
12	70	84.3	13	4 US-09-847-185-42 Sequence 42, Appl
13	70	84.3	13	4 US-09-847-949-22 Sequence 42, Appl
14	59	71.1	12	4 US-09-601-729-113 Sequence 113, Appl
15	66.3	66.3	11	4 US-09-341-982-3 Sequence 3, Appl
16	34	41.0	15	4 US-09-821-825 Sequence 5, Appl
17	33	39.8	10	4 US-09-973-608-22 Sequence 72, Appl
18	33	39.8	10	4 US-09-973-608-22 Sequence 22, Appl
19	33	39.8	10	4 US-09-616-289-22 Sequence 22, Appl
20	21	37.3	15	1 US-08-520-977-4 Sequence 4, Appl
21	28	33.7	9	US-09-318-956A-59 Sequence 59, Appl
22	28	33.7	12	4 US-09-462-118-31 Sequence 31, Appl
23	28	33.7	15	4 US-09-009-953-73 Sequence 73, Appl
24	28	33.7	15	4 US-09-009-953-241 Sequence 241, Appl
25	28	33.7	15	4 US-09-311-78A-427 Sequence 427, Appl
26	27.5	33.1	12	4 US-09-463-752A-46 Sequence 46, Appl
27	27.5	33.1	14	US-08-165-301A-6 Sequence 6, Appl

## ALIGNMENTS

RESULT 1  
US-09-036-582-23  
; Sequence 23, Application US/09036582A  
; Patent No. 5963381  
; GENERAL INFORMATION:  
; APPLICANT: van der Bruggen, Pierre  
; INVENTOR: Cornelis, Guy R.  
; TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS  
; TITLE OF INVENTION: WITH RECOMBINANT VERSINIA  
; FILE REFERENCE: 11154  
; CURRENT APPLICATION NUMBER: US-09-036-582A  
; CURRENT FILING DATE: 1998-01-05  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 23  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Human Tyrosinase peptide  
US-09-036-582-23

Query Match 100.0%; Score 83; DB 2; Length 15;  
Best Local Similarity 100.0%; Score 83; DB 2; Length 15;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DYSYLOQSDPDSFQD 15  
Db 1 DYSYLOQSDPDSFQD 15

RESULT 2  
US-09-183-706-26  
; Sequence 26, Application US/09183706  
; Patent No. 624525  
; GENERAL INFORMATION:  
; APPLICANT: Martelange, Valrie  
; INVENTOR: De Smet, Charles  
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
; FILE REFERENCE: LO461/7054  
; CURRENT APPLICATION NUMBER: US/09/183-706  
; EARLIER APPLICATION NUMBER: 1998-10-30  
; EARLIER FILING DATE: 1999-07-27  
; NUMBER OF SEQ ID NOS: 43  
; SEQ ID NO: 26  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-183-706-26

Query Match 100.0%; Score 83; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYIQLQSPDPDSFQD 15  
 Db 1 DYSYIQLQSPDPDSFQD 15

RESULT 3  
 Patent No. 6291430  
 GENERAL INFORMATION:  
     APPLICANT: Chaux, Pascal  
     APPLICANT: Vantomme, Valérie  
     APPLICANT: Stroobant, Vincent  
     APPLICANT: Boon-Falleur, Thierry  
     APPLICANT: van der Bruggen, Pierre  
     APPLICANT: Thielemans, Kris  
     APPLICANT: Cortihals, Jurgen  
     TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
     FILE REFERENCE: L0461/7052  
     CURRENT APPLICATION NUMBER: US/09/166,448  
     CURRENT FILING DATE: 1998-10-05  
     SEQ ID NO 67  
     NUMBER OF SEQ ID NOS: 81  
     SOFTWARE: FastSEQ for Windows Version 3.0  
     LENGTH: 15  
     TYPE: PROTEIN  
     ORGANISM: Homo sapiens  
 US-09-166-448-67

Query Match 100.0%; Score 83; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYIQLQSPDPDSFQD 15  
 Db 1 DYSYIQLQSPDPDSFQD 15

RESULT 4  
 Patent No. 6303156  
 GENERAL INFORMATION:  
     APPLICANT: Martelange, Valérie  
     APPLICANT: De Smet, Charles  
     APPLICANT: Boon-Falleur, Thierry  
     TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR  
     FILE REFERENCE: L0461/7054  
     CURRENT APPLICATION NUMBER: US/09/567,995  
     CURRENT FILING DATE: 2000-05-10  
     PRIOR APPLICATION NUMBER: 09/183,706  
     NUMBER OF SEQ ID NOS: 43  
     LENGTH: 15  
     TYPE: PROTEIN  
     ORGANISM: Homo sapiens  
 US-09-567-995-26

Query Match 100.0%; Score 83; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYIQLQSPDPDSFQD 15  
 Db 1 DYSYIQLQSPDPDSFQD 15

RESULT 5  
 Patent No. 6407063  
 GENERAL INFORMATION:  
     APPLICANT: Luijten, Rosalie  
     APPLICANT: Dufour, Marie-Therese  
     APPLICANT: Demotte, Nathalie  
     APPLICANT: van der Bruggen, Pierre  
     APPLICANT: Cornelis, Guy  
     APPLICANT: Stroobant, Vincent  
     APPLICANT: Lurquin, Christophe  
     APPLICANT: Boon-Falleur, Thierry  
     APPLICANT: Chaux, Pascal  
     TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL  
     FILE REFERENCE: 11727  
     CURRENT APPLICATION NUMBER: US/09/165,863  
     CURRENT FILING DATE: 1999-10-02  
     NUMBER OF SEQ ID NOS: 45  
     SEQ ID NO 23  
     LENGTH: 15  
     TYPE: PROTEIN  
     ORGANISM: Human Tyrosinase Peptide  
 US-09-165-863-23

Query Match 100.0%; Score 83; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYIQLQSPDPDSFQD 15  
 Db 1 DYSYIQLQSPDPDSFQD 15

RESULT 6  
 Patent No. 6426217  
 GENERAL INFORMATION:  
     APPLICANT: Chaux, Pascal  
     APPLICANT: Vantomme, Valérie  
     APPLICANT: Stroobant, Vincent  
     APPLICANT: Boon-Falleur, Thierry  
     APPLICANT: van der Bruggen, Pierre  
     APPLICANT: Thielemans, Kris  
     APPLICANT: Cortihals, Jurgen  
     TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
     FILE REFERENCE: L0461/7052  
     CURRENT APPLICATION NUMBER: US/09/697,884  
     CURRENT FILING DATE: 2000-10-27  
     PRIOR APPLICATION NUMBER: 09/166,448  
     PRIOR FILING DATE: 1998-10-05  
     NUMBER OF SEQ ID NOS: 81  
     SOFTWARE: FastSEQ for Windows Version 3.0  
     SEQ ID NO 67  
     LENGTH: 15  
     TYPE: PROTEIN  
     ORGANISM: Homo sapiens  
 US-09-697-884-67

Query Match 100.0%; Score 83; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYIQLQSPDPDSFQD 15  
 Db 1 DYSYIQLQSPDPDSFQD 15

RESULT 7  
 Patent No. 6426217  
 GENERAL INFORMATION:  
     APPLICANT: Chaux, Pascal  
     APPLICANT: Vantomme, Valérie  
     APPLICANT: Stroobant, Vincent  
     APPLICANT: Boon-Falleur, Thierry  
     APPLICANT: van der Bruggen, Pierre  
     APPLICANT: Thielemans, Kris  
     APPLICANT: Cortihals, Jurgen  
     TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES  
     FILE REFERENCE: L0461/7052  
     CURRENT APPLICATION NUMBER: US/09/697,884  
     CURRENT FILING DATE: 2000-10-27  
     PRIOR APPLICATION NUMBER: 09/166,448  
     PRIOR FILING DATE: 1998-10-05  
     NUMBER OF SEQ ID NOS: 81  
     SOFTWARE: FastSEQ for Windows Version 3.0  
     SEQ ID NO 67  
     LENGTH: 15  
     TYPE: PROTEIN  
     ORGANISM: Homo sapiens  
 US-09-697-884-67

Query Match 100.0%; Score 83; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYSYIQLQSPDPDSFQD 15  
 Db 1 DYSYIQLQSPDPDSFQD 15

Patent No. 6531451  
 GENERAL INFORMATION:  
 / APPLICANT: Chaux, Pascal  
 / APPLICANT: Lutten, Rosalie  
 / APPLICANT: Demotte, Nathalie  
 / APPLICANT: Deffour, Marie-Therese  
 / APPLICANT: Traversari, Catia  
 / APPLICANT: Stroobant, Vincent  
 / APPLICANT: Cornelis, Guy R.  
 / APPLICANT: Boon-Falleur, Thierry  
 / APPLICANT: Van Der Bruggen, Pierre  
 / TITLE OF INVENTION: TUMOR ANTIGENS AND CTL CLONES ISOLATED BY A NOVEL  
 / TITLE OF INVENTION: PROCEDURE  
 / FILE REFERENCE: 11727Z  
 / CURRENT APPLICATION NUMBER: US/09/289,350  
 / CURRENT FILING DATE: 1999-04-09  
 / PRIOR APPLICATION NUMBER: 09/165,863  
 / PRIOR FILING DATE: 1998-10-02  
 / NUMBER OF SEQ ID NOS: 49  
 / SEQ ID NOS: 22  
 / LENGTH: 15  
 / TYPE: PRT  
 / ORGANISM: Human Tyrosinase Peptide  
 US-09-289-350-23

Query Match 100.0%; Score 83; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
 Matches 15; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 DYSYQLQSDPDSFQD 15  
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 Db 1 DYSYQLQSDPDSFQD 15

---

RESULT 8  
 US-09-574-749B-25  
 / GENERAL INFORMATION:  
 / Patent No. 6548299  
 / APPLICANT: ROSENZWEIG, Michael  
 / APPLICANT: PYKETT, Mark J.  
 / APPLICANT: SCADDEN, David T.  
 / APPLICANT: POZNANSKY, Mark C.  
 / TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION  
 / TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL  
 / TITLE OF INVENTION: DEVICES  
 / FILE REFERENCE: CL005/7012/KA/ERG  
 / CURRENT APPLICATION NUMBER: US/09/574,749B  
 / CURRENT FILING DATE: 2002-05-31  
 / PRIOR APPLICATION NUMBER: US 60/107,972  
 / PRIOR FILING DATE: 1998-11-12  
 / PRIOR APPLICATION NUMBER: PCT/US99/26795  
 / PRIOR FILING DATE: 1999-11-12  
 / PRIOR APPLICATION NUMBER: US 09/524,749  
 / PRIOR FILING DATE: 2000-05-18  
 / NUMBER OF SEQ ID NOS: 58  
 / SOFTWARE: FastSEQ for Windows Version 3.0  
 / LENGTH: 15  
 / TYPE: PRT  
 / OTHER INFORMATION: Homo Sapiens source  
 / FEATURE:  
 / US-09-574-749B-25

Query Match 100.0%; Score 83; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
 Matches 15; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 DYSYQLQSDPDSFQD 15  
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 Db 1 DYSYQLQSDPDSFQD 15

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RESULT 9  
 US-09-318-141-23  
 / Sequence 23, Application US/09318141  
 / Patent No. 6602506  
 / GENERAL INFORMATION:  
 / APPLICANT: van der Bruggen, Pierre  
 / APPLICANT: Cornelis, Guy R.  
 / TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS  
 / TITLE OF INVENTION: WITH RECOMBINANT YERSINIA  
 / FILE REFERENCE: 11154  
 / CURRENT APPLICATION NUMBER: US/09/318,141  
 / CURRENT FILING DATE: 1999-05-25  
 / EARLIER APPLICATION NUMBER: US 09/036,582  
 / EARLIER FILING DATE: 1998-03-06  
 / NUMBER OF SEQ ID NOS: 39  
 / SOFTWARE: PatentIn Ver. 2.0  
 / SEQ ID NO: 23  
 / LENGTH: 15  
 / TYPE: PRT  
 / ORGANISM: Human Tyrosinase Peptide  
 US-09-318-141-23

Query Match 100.0%; Score 83; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
 Matches 15; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 DYSYQLQSDPDSFQD 15  
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 Db 1 DYSYQLQSDPDSFQD 15

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RESULT 10  
 US-09-169-717E-29  
 / Sequence 29, Application US/09169717E  
 / Patent No. 6667037  
 / GENERAL INFORMATION:  
 / APPLICANT: Ooms, Annie  
 / APPLICANT: Degiovanni, Gerard  
 / APPLICANT: Morel, Sandra  
 / APPLICANT: Van den Bynde, Benoit  
 / APPLICANT: Boon-Falleur, Thierry  
 / TITLE OF INVENTION: Isolater Peptides Which Bind To HLA-B35 Molecules,  
 / TITLE OF INVENTION: Larger Peptides Which Contain These Nucleic Acid  
 / TITLE OF INVENTION: Molecules Encoding Peptides, And Uses Thereof  
 / FILE REFERENCE: IUD5561  
 / CURRENT APPLICATION NUMBER: US/09/169,717E  
 / CURRENT FILING DATE: 1998-10-09  
 / NUMBER OF SEQ ID NOS: 39  
 / SEQ ID NO: 29  
 / LENGTH: 15  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 / FEATURE:  
 / US-09-169-717E-29

Query Match 100.0%; Score 83; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
 Matches 15; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 DYSYQLQSDPDSFQD 15  
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 Db 1 DYSYQLQSDPDSFQD 15

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RESULT 11  
 US-09-902-516-42  
 / Sequence 42, Application US/08902516  
 / Patent No. 5891412  
 / GENERAL INFORMATION:  
 / APPLICANT: Soo Hoo, William

TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
 TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CAMPBELL & FLORES, LLP  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: United States  
 ZIP: 92121  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 APPLICATION NUMBER: US/08/902,516  
 FILING DATE: 29-JUL-1997  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-IM 2442  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9001  
 TELEFAX: (619) 535-8949  
 INSEQUENCE FOR SEQ ID NO: 42:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide

RESULT 12  
 US-09-847-185-42  
 Sequence 42, Application US/09847185  
 Parent No. 6,824,07  
 GENERAL INFORMATION:  
 APPLICANT: SOO HOO, William  
 TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
 COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CAMPBELL & FLORES, LLP  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: United States  
 ZIP: 92121  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/847-185  
 FILING DATE: 01-May-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/201,931  
 FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-IM 2442  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9001  
 TELEFAX: (619) 535-8949  
 INFORMATION FOR SEQ ID NO: 42:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 42:  
 US-09-847-185-42  
 Query Match 84.3%; Score 70; DB 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1..9e-05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 SYLQDSDPDSDFD 15  
 Db 1 SYLQDSDPDSDFD 13  
 RESULT 13  
 US-09-601-729-113  
 Sequence 113, Application US/09601729  
 Patent No. 6,830,52  
 GENERAL INFORMATION:  
 APPLICANT: THIAM, KADER  
 APPLICANT: AUBRIAL, CLAUDE  
 APPLICANT: GRAS-MASSE, HELENE  
 APPLICANT: LOING, ESTELLE  
 APPLICANT: VERNAERDE, CLAUDIE  
 APPLICANT: GUILLET, JEAN GERARD  
 TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES  
 THEREOF IN PHARMACEUTICAL COMPOSITIONS  
 FILE REFERENCE: USB-97-AU-IN  
 CURRENT APPLICATION NUMBER: US/09/501,729  
 PRIORITY APPLICATION NUMBER: PCT/FR99/00259  
 PRIORITY FILING DATE: 1999-02-05  
 PRIORITY APPLICATION NUMBER: 98 01439  
 PRIORITY FILING DATE: 1998-02-06  
 NUMBER OF SEQ ID NOS: 281  
 SOFTWARE: Patentin Ver. 2.1  
 SEQ ID NO 113  
 LENGTH: 13  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 OTHER INFORMATION: Peptide  
 OTHER INFORMATION: Peptide  
 US-09-601-729-113  
 Query Match 84.3%; Score 70; DB 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1..9e-05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 SYLQDSDPDSDFD 15  
 Db 1 SYLQDSDPDSDFD 13  
 RESULT 14  
 US-09-341-982-3  
 Sequence 3, Application US/09341982  
 Patent No. 6,558,671  
 GENERAL INFORMATION:  
 APPLICANT: SLINGUFF, Craig L.  
 APPLICANT: HUNT, Donald F.  
 APPLICANT: ENGELHARD, Victor H.

; APPLICANT: KITTELSEN, David  
 ; TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED  
 ; TITLE OF INVENTION: CYTOTOXIC LYMPHOCYTES, AND USES THEREFOR  
 ; FILE REFERENCE: SLINGLUFF=3B  
 ; CURRENT APPLICATION NUMBER: US/09/341,982  
 ; CURRENT FILING DATE: 1999-09-20  
 ; EARLIER APPLICATION NUMBER: PCT/US98/01592  
 ; EARLIER FILING DATE: 1998-01-29  
 ; EARLIER APPLICATION NUMBER: 60/037,781  
 ; EARLIER FILING DATE: 1997-01-31  
 ; NUMBER OF SEQ ID NOS: 104  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 3  
 ; LENGTH: 12  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Fragment of  
 ; OTHER INFORMATION: human protein  
 US-09-341-982-3

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Query Match 71.1%; Score 59; DB 4; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.0011; Indels 0; Gaps 0;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 LDQSDPDSFQD 15  
 Db 1 LDQSDPDSFQD 11

RESULT 15  
 US-09-341-982-5  
 ; Sequence 5, Application US/09341,982  
 ; Patent No. 6558671  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SLINGLUFF, Craig L.  
 ; APPLICANT: TONT, Donald F.  
 ; APPLICANT: ENGELHARD, Victor H.  
 ; APPLICANT: KITTELSEN, David  
 ; TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED  
 ; TITLE OF INVENTION: CYTOTOXIC LYMPHOCYTES, AND USES THEREFOR  
 ; CURRENT APPLICATION NUMBER: US/09/341,982  
 ; CURRENT FILING DATE: 1999-09-20  
 ; EARLIER APPLICATION NUMBER: PCT/US98/01592  
 ; EARLIER FILING DATE: 1998-01-29  
 ; EARLIER APPLICATION NUMBER: 60/037,781  
 ; EARLIER FILING DATE: 1997-01-31  
 ; NUMBER OF SEQ ID NOS: 104  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 5  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Fragment of  
 ; OTHER INFORMATION: human protein  
 US-09-341-982-5

Query Match 66.3%; Score 55; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.0045;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 6 QDSDPDSFQD 15  
 Db 1 QDSDPDSFQD 10